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FIG.1A. NUCLEOTIDE SEQUENCE OF THE PIV-3 F GENE (PCR-AMPLIFIED)

AAGTCAATACCAACAACATAATTAGCAGTCAATACGTGCAAGAAACAAGAAAGAGATTCAA
TTCAGTTATGGTTGTTGATAAATCGTCAGTATGCACGTTCTTGTCTTCTCTAAGTT 60
10 20 30 40 50

AAAGCTAAATAAGAGAAATCAAAACAAGGATATAGAACACCCGGAACAACAATCAAAA
TTTCGATTTATTTCTCTTTAGTTTGTCTTCCATATCTTGTGGGCTTGTGTTTGTAGTTTT 120
70 80 90 100 110

CATCCAAATCCATTTTAAACAATAATCCAAAAGAGACCCGGCAACAACAAGCACCAAC
GTAGGTTAGGTAAATTTGTTTAAAGGTTTCTCTGGCCGTTGTGTTGTTGTTGTTG 180
130 140 150 160 170

MET PRO THR LEU ILE LEU LEU ILE ILE THR THR MET ILE MET ALA SER SER CYS GLN
ACAAATGCCAACTTTAATACTGCTAATTTACACAACAATGATTATGGCATCTTCTCTGCCAA
TGTTACGGTTGAAATTTATGACGATTAAATAATGTTGTTACTAATAACCGTAGAAGGACGGTT 240
190 200 210 220 230 240

ILE ASP ILE THR LYS LEU GLN HIS VAL GLY VAL LEU VAL ASN SER PRO LYS GLY MET LYS
ATACATATCACAAACTACAGCATGTAGGTGTTATTTGGTCAACAGTCCCAAGGGATGAAG
TATGTAATAGTGTGTTGATGTCGTACATCCACATAACCCAGTTGTACAGGGTTTCCCTACTTC 300
250 260 270 280 290 300

ILE SER GLN ASN PHE GLU THR ARG TYR LEU ILE LEU SER LEU ILE PRO LYS ILE GLU ASP
ATATCACAAACTTCGAAACAAGATATCTAAATTTTGAGCCCTCATACCAAAAATAGAAGAC
TATAGTGTTTTTGAAAGCTTTGTTCTATAGATTAAACTCGGAGTATGGTTTTTATCTTCTG 360
310 320 330 340 350 360

SER ASN SER CYS GLY ASP GLN GLN ILE LYS GLN TYR LYS ARG LEU LEU ASP ARG LEU ILE
TCTAACTCTTGTGGTGACCAACAGATCAACAATAACAAGAGGTTATTGGATAGACTGATC
AGATTGAGAACACCACTGGTTGTCTAGTTTGTGTTATGTTCTCCAATAACCTATCTGACTAG 420
370 380 390 400 410 420

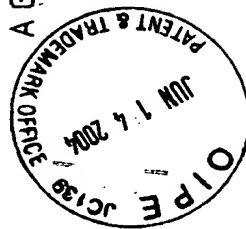


FIG. 1B.

ILE PRO LEU TYR ASP GLY LEU ARG LEU GLN LYS ASP VAL ILE VAL **THR** ASN GLN GLU SER
 ATCCCTCTATATGATGGATTAAAGATTACAGAAAGATGTGATAGTAAACCCAATCAAGAATCC
 TAGGGAGATATACTACCTAAATTCTAATGTCTTTCTACACATATCATTTGGTTAGTTCTTAGG 480
 430 440 450 460 470 480

F2-F1 CLEAVAGE SITE

ASN GLU ASN THR ASP PRO ARG THR **ARG** **SER** PHE GLY GLY VAL ILE GLY THR ILE ALA
 AATGAAACACACTGATCCAGAACAAAGACGATCCCTTTGGAGGGGTAAATTGGGAACCATTTGCT
 TTACTTTTGTGACTAGGGTCTTGTCTGCTAGGAAACCTCCCCATTAACCTTGGTAACGA 540
 490 500 510 520 530 540

LEU GLY VAL ALA THR SER ALA GLN ILE THR ALA ALA VAL ALA LEU VAL GLU ALA LYS GLN
 CTGGGAGTAGCAACCTCAGCACAAATTACAGCGGCAGTTGCTCTGGTTGAAGCCCAAGCAG
 GACCCCTCATCGTTGGAGTCGTGTTTAAATGTCGCCGTCACACGAGACCAACTTCGGTTCGTC 600
 550 560 570 580 590 600

ALA **LYS** SER ASP ILE GLU LYS LEU LYS GLU ALA ILE ARG ASP THR ASN LYS ALA VAL GLN
 GCAAAATCACACATCGAATAAATCAAGAAAGCAATCAGGGACACAAACAAGCAGTGTCAG
 CGTTTTAGTGTTAGCTTTTGGAGTTTCTTCGTTAGTCCCTGTGTTTGGTTTCGTCACGTC 660
 610 620 630 640 650 660

SER VAL GLN SER SER ILE GLY ASN LEU ILE VAL ALA ILE LYS SER VAL GLN ASP TYR VAL
 TCAGTTTCAGAGCTCTATAGGAAATTTAATAGTAGCAATTAAATCAGTCCCAAGATTATGTC
 AGTCAAGTCTCGAGATATCCCTTTAAATTTATCATCGTTAAATTTAGTCAAGGTTCTAATACAG 720
 670 680 690 700 710 720

ASN **ASN** GLU ILE VAL PRO SER ILE ALA ARG LEU GLY CYS GLU ALA ALA GLY LEU GLN LEU
 AACAAACGAAATCGTGCCATCGATTGCTAGACTAGGTTGTGAAGCAGCAGGACTTCAATTA
 TTGTTGCTTTAGCACGGTAGCTAACGATCTGATCCAAACACTTTCGTCGCTGAAAGTTAAT 780
 730 740 750 760 770 780

GLY ILE ALA LEU THR GLN HIS TYR SER GLU LEU THR ASN ILE PHE GLY ASP ASN ILE GLY
 GGAAATTGCAATTAAACACAGCATTAATCTCAGAAATTAAACAACATATTTGGTGATAACATAGGA
 CCTTAACGTAAATTGTGTCGTAATGAGTCTTAATTTGTTGTATAAACCACTATTGTATCCT 840
 790 800 810 820 830 840



FIG.1C.

SER LEU GLN GLU LYS GLY ILE LYS LEU GLN GLY ILE ALA SER LEU TYR ARG THR ASN ILE
TCGTTACAAGAAAGGAATAAAATTACAAGGTATAGCATCATATTATACCGCACAAATATC
AGCAATGTTCTTTTTCCTTATTTTAATGTTCCCATATCGTAGTAATAATGGCGTGTTTAG
850 860 870 880 890 900

THR GLU ILE PHE THR THR SER THR VAL ASP LYS TYR ASP ILE TYR ASP LEU LEU PHE THR
ACAGAAATATTACACAACATCAACAGTTGATAAATATGATATCTATGATCTATTATTACA
TGTCTTTATAAAGTGTTGTAGTTGTCAACTATTTTATCTATAGATACTAGATAATAAATGT
910 920 930 940 950 960

GLU SER ILE LYS VAL ARG VAL ILE ASP VAL ASP LEU ASN ASP TYR SER ILE THR LEU GLN
GAATCAATAAAGGTGAGAGTTATAGATGTTGATTTGAATGATTACTCAATCACCCCTCCAA
CTTAGTTATTTCCCACTCTCAATATCTACAACCTAACTTACTAATGAGTTAGTGGGAGGTT
970 980 990 1000 1010 1020

VAL ARG LEU PRO LEU LEU THR ARG LEU LEU ASN THR GLN ILE TYR LYS VAL ASP SER ILE
GTCAGACTCCCTTTTATTAACTAGGCTGCTGAACTGAGATCTACAAGTAGATTCCATA
CAGTCTGAGGGAAATAATTGATCCGACGACTTGTGAGTCTAGATGTTTTCATCTAAGGTAT
1030 1040 1050 1070 1080

SER TYR ASN ILE GLN ASN ARG GLU TRP TYR ILE PRO LEU PRO SER HIS ILE MET THR LYS
TCATATAATATCCAAACAGAGAAATGGTATATCCCTCTTCCAGCCATATCATGACGAAA
AGTATATTATAGGTTTGTCTCTTACCATAATAGGGAGAAAGGTCGGTATAGTACTGCTTT
1090 1100 1110 1120 1130 1140

GLY ALA PKE LEU GLY GLY ALA ASP VAL LYS GLU CYS ILE GLU ALA PHE SER SER TYR ILE
GGGGCATTTCTAGGTGGAGCAGATGTCAAGGAATGTATAGAACATTTCAGCAGTTATATA
CCCCGTAAAGATCCACCTCGTCTACAGTTTCCTTACATATCTTCGTAAGTCGTCAATATAT
1150 1160 1170 1180 1190 1200

CYS PRO SER ASP PRO GLY PHE VAL LEU ASN HIS GLU KET GLU SER CYS LEU SER GLY ASN
TGCCCTTCTGATCCAGGATTTGTACTAAACCATGAATGGAGAGCTGCTTATCAGGAAAC
ACGGGAAGACTAGGTCCTAAACATGATTTGGTACTTTACCTCTCGACGAAATAGTCCCTTG
1210 1220 1230 1240 1250 1260



FIG.1D. ILE SER GLN CYS PRO ARG THR [THR] VAL [THR] SER ASP ILE VAL PRO ARG TYR ALA PHE VAL
ATATCCCAATGTCCAAAGAACCCACGGTCAATCAGACATTTGTTCCAAAGATATGCAATTCGTC
TATAGGGTTACAGGTTCTTGGTGCCAGTGAGTCTGTACAAAGGTTCTATACGTAAGCAG 1270 1280 1290 1300 1310 1320

ASN GLY GLY VAL VAL ALA ASN CYS ILE THR THR THR CYS THR CYS ASN GLY ILE [ASP] ASN
AATGGAGGAGTGTTGCAAACTGTATAAACAACCCCTGTACATGCAACGGAATCGACAAT
TTACCTCCTCACCAACGTTTGACATATTGTTGGTGGACATGTACGTTGCCCTTAGCTGTTA 1330 1340 1350 1360 1370 1380

ARG ILE ASN GLN PRO PRO ASP GLN GLY VAL LYS ILE THR THR HIS LYS GLU CYS ASN THR
AGAAATCAATCAACCACTGATCAAGGAGTAAATAATTATAACACATAAAGAAATGTAATACA
TCTTAGTTAGTTGGTGGACTAGTTCCCTCATTTTAAATATTGTGTATTTCTTACATTATGT 1390 1400 1410 1420 1430 1440

ILE GLY ILE ASN GLY MET LEU PHE ASN THR ASN LYS GLU GLY THR LEU ALA PHE TYR THR
ATAGGTATCAACGGAATGCTGTTCATAATACAAATAAAGAGGAACCTCTTGCAATCTACACA
TATCCATAGTTGCCCTTACGACAAGTTATGTTTATTTCTTCCCTTGAGAACGTAAGATGTGT 1450 1460 1470 1480 1490 1500

PRO ASN ASP ILE THR LEU ASN ASN SER VAL ALA LEU ASP PRO ILE ASP ILE SER ILE GLU
CCAAATGATATAACACTAAATAATTCTGTGCACTTGATCCAAATTGACATATCAATCGAG
GGTTTACTATATTGTGATTTTAAAGACAACGTAACCTAGGTTAACTGTATAGTTAGCTC 1510 1520 1530 1540 1550 1560

LEU ASN LYS ALA LYS SER ASP LEU GLU GLU SER LYS GLU TRP ILE ARG ARG SER ASN GLN
CTTAACAAGCCAAATCAGATCTAGAAAGAAATCAAAAGAAATGGATAAGAAAGTCAAAATCAA
GAATTGTTTCGGTTTAGTCTAGATCTTCTTAGTTTCTTACCTATTCTTCCAGTTTAGTT 1570 1580 1590 1600 1610 1620

LYS LEU ASP SER ILE GLY ASN TRP HIS GLN SER SER THR THR ILE ILE ILE [LE] LEU ILE
AACTAGATTCTATTGGAAACTGGCATCAATCTAGCACTACAATCAATAATTATTTTAATA
TTTGATCTAAGATAACCTTTGACCGTAGTTAGATCGTGAATTAATAAAATTAT 1630 1640 1650 1660 1670 1680



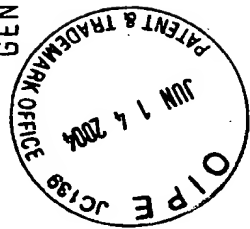
FIG.1E

MET ILE ILE ILE LEU PHE ILE ILE ASN VAL THR ILE ILE THR ILE ALA ILE LYS TYR TYR
 ATGATCATTATATTGTTTATATAATTAAATGTAACGATAATTACAAATTGCAATTAAAGTATTAC
 TACTAGTAATATAACAATAATTAATTACATTGCTATTAAATGTTAACGTTAAATTCAATAATG 1740
 1690 1700 1710 1720 1730

ARG ILE GLN LYS ARG ASN ARG VAL ASP GLN ASN ASP LYS PRO TYR VAL LEU THR ASN LYS
 AGAATTCAAAAGAGAAATCGAGTGGATCAAAATGACAAGCCATATGTACTAACAAACAAA
 TCTTAAGTTTTCTCTTTAGCTCACCTAGTTTTTACTGTTTCGGTATACATGATTGTTGTTT 1800
 1750 1760 1770 1780 1790

TGACATATCTATAGATCATTAGATATTAAATTTAATAAAACTT
 ACTGTATAGATATCTAGTAATCTATAAATTTAATATTTTGGAA 1840
 1810 1820 1830 1840

NUCLEOTIDE SEQUENCE OF THE PIV-3 F GENE. THE cDNA SEQUENCE IS SHOWN IN THE PLUS (mRNA) STRAND SENSE IN THE 5' TO 3' DIRECTION. THE SIGNAL PEPTIDE (SP) AND THE TRANSMEMBRANE (TM) ANCHOR DOMAIN ARE UNDERLINED. THE PREDICTED F2-F1 CLEAVAGE SITE IS INDICATED BY THE ARROW (↓). AMINO ACIDS DIFFERING FROM THE PUBLISHED PRIMARY SEQUENCE OF THE PROTEIN ENCODED BY THE PIV-3 F GENE ARE BOXED.



RESTRICTION MAP OF THE PIV-3 F GENE

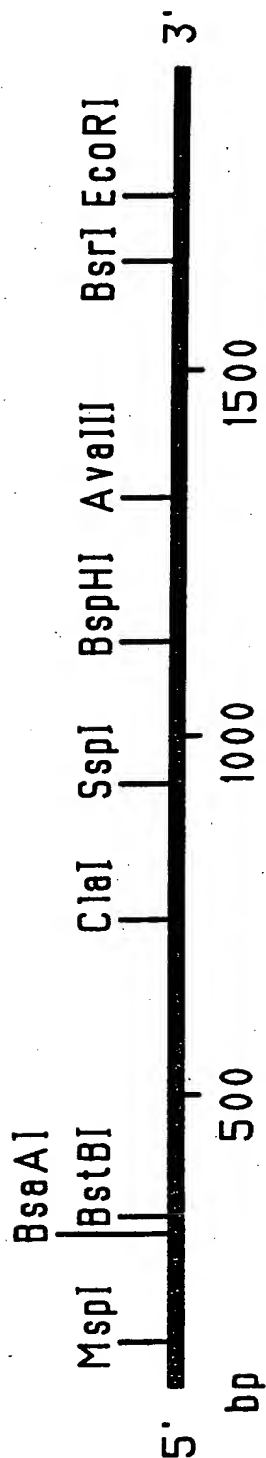


FIG.2.



FIG.3A.

NUCLEOTIDE SEQUENCE OF THE PIV-3 HN GENE.

5' AGACAAATCCAAATTCGAGATGGAAATACTGGAAAGCATACCAATCACGGAAGGATGCTGG
 TCTGTTTAGGTTTAAGCTCTACCTTATGACCTTTCGTAATGGTTAGTGCCCTTCCCTACGACC
 10 20 30 40 50 60
 MET GLU TYR TRP LYS HIS THR ASN HIS GLY LYS ASP ALA GLY
 ASN GLU LEU GLU THR SER MET ALA THR [ASN] GLY ASN LYS [LEU] THR ASN LYS ILE THR TYR
 CAATGAGCTGGAGACGTCCTCATGGCTACTAATGGCAACCAAGCTCACCAATAAGATAACATA
 GTTACTCGACCCTCTGCAGGTACCGATGATTACCGTTGTTTCGAGTGGTATTCTATTGTAT
 70 80 90 100 110 120
 ILE LEU TRP THR ILE ILE LEU VAL LEU SER ILE VAL PHE ILE ILE VAL LEU ILE ASN
 TATATTATGGACAAATAATCCTGGTGTATTATTCATAATAGTCTTTCATCATAGTGCTAATTAA
 ATATAATACCTGTATTATTAGGACCACCAATAATAATAGTTATTCAGAAAGTAGTATTCACGATTAAAT
 130 140 150 160 170 180
 SER ILE LYS SER GLU LYS ALA HIS GLU SER LEU LEU GLN ASP [ILE] ASN ASN GLU PHE MET
 TTCCCATCAAAGTGAAAGGCTCATGAATCATTTGCTGCAAGACATATAAATAATGAGTTTAT
 AAGGTAGTTTTCACCTTTTCCGAGTACTTAGTAACGACGTTCTGTATTTATTACTCAAATA
 190 200 210 220 230 240
 GLU [ILE] THR GLU LYS ILE GLN MET ALA SER ASP ASN [THR] ASN ASP LEU ILE GLN SER GLY
 GGAAATTACAGAAAGATCCCAAATGGCATCGGATAATACCAATGATCTAATAACAGTCAGG
 CCTTTAATGTCTTTTCTAGGTTTACCGTAGCCCTATTATGGTTACTAGATTATGTCAGTCC
 250 260 270 280 290 300
 VAL ASN THR ARG LEU LEU THR ILE GLN SER HIS VAL GLN ASN TYR ILE PRO ILE SER LEU
 AGTGAAATACAAAGGCTTCTTTACAAATTCAGAGTTCATGTCCAGAAATTATATACCAATATCCT
 TCACCTTATGTTCCGAAGAATGTTAAGTCTCAGTACAGGCTTATAATATGTTATAGTGA
 310 320 330 340 350 360



THR GLN GLN MET SER ASP LEU ARG LYS PHE ILE SER GLU ILE THR ILE ARG ASN ASP ASN
GACACAAACAGATGTCAGATCTTAGGAAATTTCATTAGTGAAATTACAAATTAGAAATGATAA
CTGTGTTGTTACAGTCTAGAAATCCCTTTAAGTAATCACCTTTAATGTTAAATCTTTACTATT
370 380 390 400 410 420

[GLN] GLU VAL [LEU] PRO GLN ARG ILE THR HIS ASP [VAL] GLY ILE LYS PRO LEU ASN PRO ASP
TCAAGAAAGTGCTGCTGCCACAAGAAATAACACATGATGTGGGTATAAAACCCTTTAAATCCAGA
AGTTCTTTCACGACGGGTGTTTCTTATTGTGTACTACACCCCAATTTTGGGAAATTTAGGTCT
430 440 450 460 470 480

ASP PHE TRP ARG CYS THR SER GLY LEU PRO SER LEU MET LYS THR PRO LYS ILE ARG LEU
TGATTTTGGAGATGACGCTCTGGTCTTCCATCTTTAATGAACAACTCCAAATAAAGGTT
ACTAAACACCTCTACGTGCAGACCCAGAAAGGTAGAAATTTACTTTTGGAGGTTTATTCCAA
490 500 510 520 530 540

MET PRO GLY PRO GLY LEU LEU ALA MET PRO THR THR VAL ASP GLY CYS [ILE] ARG THR PRO
AATGCCAGGGCCGGGATTATTAGCTATGCCAACGACTGTGTGATGGCTGTATTCAGAACTCC
TTACGGTCCCGGCCCTAATAATCGATACGGGTGCTGACAACTACCGACATAGTCTTGAGG
550 560 570 580 590 600

SER LEU VAL ILE ASN ASP LEU ILE TYR ALA TYR THR SER ASN LEU ILE THR ARG GLY CYS
GTCCTTAGTTATAAATGATCTGATTATTGCTTTATACCTCAAAATCTAAATTAATCGAGGTTG
CAGGAATCAATATTACTAGACTAAATACGAAATATGGAGTTTAGATTAAATGAGCTCCAAC
610 620 630 640 650 660

GLN ASP ILE GLY LYS SER TYR GLN VAL LEU GLN ILE GLY ILE THR VAL ASN SER ASP
TCAGGATATAGGAAATCATATCAAGTCTTACAGATAGGGATAAATAACTGTAAACTCAGA
AGTCCCTATATCCCTTTTAGTATAGTTTCAGAAATGCTATATCCCTATTATTGACATTTGAGTCT
670 680 690 700 710 720

LEU VAL PRO ASP LEU ASN PRO ARG ILE SER HIS THR PHE ASN ILE ASN ASP ARG LYS
CTTGGGTACCTGACTTAAATCCCAGGATCTCTCATACTTTTAACATAAATGACAAATAGGAA
GAACCATGGACTGAATTTAGGGTCCCTAGAGAGTATGAAAATTGTTATTACTGTTATCCTT
730 740 750 760 770 780

FIG. 3B.





SRE CYS SER LEU ALA LEU LEU ASN THR ASP VAL TYR GLN LEU CYS SER THR PRO LYS VAL
GTCA TGTTCTCTAGCACCTCCCTAAATACAGATGTATATCAACTGTGTTCAACTCCCAAAGT 840
CAGTACAAGAGATCGTGAGGATTTATGTCTACATATAGTTGACACAAAGTTGAGGGTTTCA 830
790 800 810 820 830

ASP GLU ARG SER ASP TYR ALA SER SER GLY ILE GLU ASP ILE VAL LEU ASP ILE VAL ASN
TGATGAAGAAGATCAGATTATGCAATCAGGCATAGAAAGATATTGTACTTGTATATTGTCAA
ACTACTTTCTAGTCTAATACGTAGTAGTCCGTATCTTCTATAACATGAACTATAACAGTT 900
850 860 870 880 890 900

TYR ASP GLY SER ILE SER THR THR ARG PHE LYS ASN ASN ILE SER PHE ASP GLN PRO
TTATGATGGCTCAATCTCAACAACAAGATTTAAGAAATAATAACATAAAGCTTTGTATCAACC
AATACTACCAGGTTAGAGTTGTTGTTCTAAATTCTTATTATTGTAATTCGAAACTAGTTGG 960
910 920 930 940 950 960

TYR ALA ALA LEU TYR PRO SER VAL GLY PRO GLY ILE TYR TYR LYS GLY LYS ILE PHE
TTATGCTGCACTATACCCATCTGTGGACCAAGGATATACCTACAAAGGCAAAATAATATT
AATACGACGTGATATGCGGTAGACCAACCCTGGTCCCTATATGATGTTTCCGTTTATTATAA 1020
970 980 990 1000 1010 1020

LEU GLY TYR GLY GLY LEU GLU HIS PRO ILE ASN GLU ASN **VAL** ILE CYS ASN THR THR GLY
TCTCGGGTATGGAGGTCTTGAAACATCCCAATAAATGAGGAATGTAAATCTGCAACACAACTGG
AGAGCCCATACCTCCAGAACTTGTAGGTATTACTCTTACATTAGACGTTGTGTTGACC 1080
1030 1040 1050 1060 1070 1080

CYS PRO GLY LYS THR GLN ARG ASP CYS ASN GLN ALA SER HIS SER PRO TRP PHE SER ASP
GTGTCGCCGGGAAACACAGAGAGACTGCAATCAGGCATCTCATAGTCCCATG6TTTTCAGA
CACAGGGCCCTTTTGTGTCCTCTGACGTTAGTCCGTAGAGTATCAGGTACCAAAAGTCT 1140
1100 1110 1120 1130 1140

ARG ARG MET VAL ASN SER ILE VAL VAL ASP LYS GLY LEU ASN SER ILE PRO LYS LEU
TAGGAGGATGGTCAACTCTATCATTTGTTGTGACAAAGGCTTAAACTCAATTCCAAATTT
ATCCTCCTACCAAGTTGAGATAGTAACAACAACCTGTTTCCGAAATTTGAGTTAAGGTTTAA 1200
1150 1160 1170 1180 1190 1200

FIG.3C.

LYS VAL TRP THR ILE SER MET ARG GLN ASN TYR TRP GLY SER GLU GLY ARG LEU LEU LEU
G A A G G T A T G G A C C G A T A T C T A T G A G A C A G A A T T A C T G G G G T C A G A A G G A A G G T T A C T T C T
C T T C C A T A C C T G C T A T A G A T A C T C T G T C T T A A T G A C C C C C A G T C T T C C T T C C A A T G A A G A
1210 1220 1230 1240 1250 1260

LEU GLY ASN LYS ILE TYR ILE TYR THR ARG SER THR SER TRP HIS SER LYS LEU GLN LEU
ACTAGGTAACAAGATCTATATATACAAAGATCCACAAAGTTGGCATAGCAAGTTACCAATT
TGATCCATTGTTCTAGATATATATGTTCTAGGTGTTCAACCCTATTCGTTCAATGTTAA
1270 1280 1290 1300 1310 1320

GLY ILE ILE ASP ILE THR ASP TYR SER ASP ILE ARG ILE LYS TRP THR TRP HIS ASN VAL
 AGGAAATAATTGATAATTACTGATTACAGTGATATAAGGATAAAATGGACATGGCATAAATGT
 TCCTTATTAACTATAATGACTAATGTCCTACTATAATTCCTATTTTACCTGTACCGTATTACA
 1330 1340 1350 1360 1370 1380

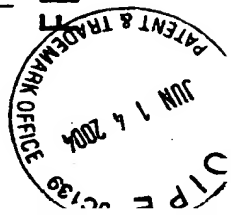
LEU SER ARG PRO GLY ASN ASN GLU CYS PRO TRP GLY HIS SER CYS PRO ASP GLY CYS ILE
GCTATCAAGACCAAGGAACCAATGAAATGTCCTCATGGGACATTCATATGTCACAGATGGGATGTAT
CGATAGTTCTGGTCCCTTTGTTACTTACAGGTACCCCTGTAAGTACAGGTCCTACCTACATA
1390 1400 1410 1420 1430 1440

[illegible]

ILE	LEU	ASP	SER	GLN	LYS	SER	ARG	VAL	ASN	PRO	VAL	ILE	THR	TYR	SER	THR	<div style="border: 1px solid black; padding: 0 2px;">ALA</div>	THR	GLU
CAT	ATT	GAT	TCA	CAA	AAA	TTC	GAG	AGT	GAA	CCC	AGT	CAT	AAC	TTA	CTC	AAC	AGC	AAC	CGA
GTA	TAA	TCT	AAG	TGTT	TTT	TAG	CTCT	CAC	TCT	GCG	TCA	GTA	TAT	TGA	ATT	GAG	TTG	TCG	TGG
						1520					1530					1540			1560

ARG VAL ASN GLU LEU ALA ILE **ARG** ASN ARG THR LEU SER ALA GLY TYR THR THR SER
AAGAGTAAACGAGCTGGCCATCCGAAACAGAACACTCTCAGCTGGATATATACAACAACAAG
TTCTCATTTGCTCGACCGGTAAGGCTTTGTCTTGTGAGAGTCCGACCTATATGTGTGTTGTTTC
1570 1580 1590 1600 1610 1620
E16.3D.

FIG. 3D.



CYS ILE THR HIS TYR ASN LYS GLY TYR CYS PHE HIS ILE VAL GLU ILE ASN GLN LYS SER
 CTGCATCACACACTATAACAAGGATATTGTTTTCATATAGTAGAATAAATTCAGAAAAG
 GACGTAGTGTGATATTGTTTCCCTATAAACAAGTATATCATCTTTATTTAGTCTTTTC
 1630 1640 1650 1660 1670 1680

LEU ASN THR LEU GLN PRO MET LEU PHE LYS THR GLU VAL PRO LYS SER CYS SER ***
 CTTAAACACACTTCAACCCCATGTTGTTCAAGACAGAGGTTCCCAAAGCTGCAGTTAATC
 GAATTTGTTGTAAGTTGGGTACACAAGTTCTCTCCCAAGGTTTTCGACGTCAAATTAG
 1690 1700 1710 1720 1730 1740

ATAATTAAACCGCAATATGCAATTAAACCTATCTATATAACAAGTATATGATAAGTAATCAGC
 TATTAAATTGGCGTTATACGTAATTGGATAGATATTATGTTCAATATCTATTATTAGTCG
 1750 1760 1770 1780 1790 1800

AATCAGACAAATAGACAAAAGGGAATATAAAAA
 TTAGTCTGTTATCTGTTTTCCTTTTATATTTT
 1810 1820 1830

NUCLEOTIDE SEQUENCE OF THE PIV-3 HN GENE. THE cDNA SEQUENCE
 IS SHOWN IN THE PLUS (mRNA) STRAND SENSE IN THE 5' TO 3'
 DIRECTION. THE TRANSMEMBRANE (TM) ANCHOR DOMAIN IS UNDERLINED. AMINO ACIDS
 DIFFERING FROM THE PUBLISHED PRIMARY SEQUENCE OF THE PROTEIN ENCODED BY THE PIV-3
 HN GENE ARE BOXED.

FIG.3E.



RESTRICTION MAP OF THE PIV-3 HN GENE

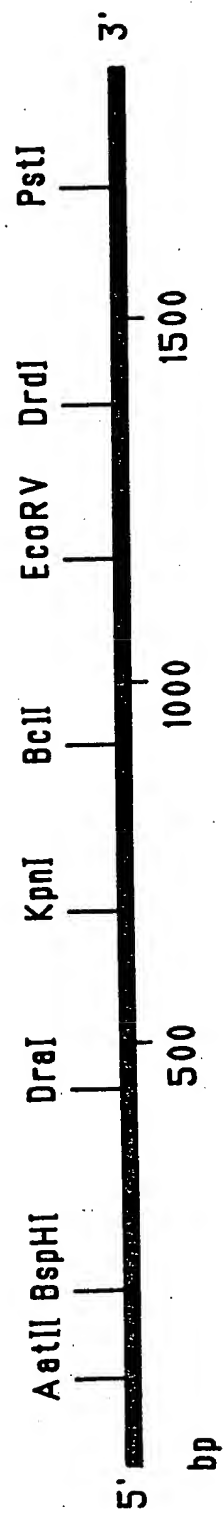


FIG.4.



FIG.5A.

NUCLEOTIDE SEQUENCE OF THE RSV F GENE.

5' MET GLU LEU [PRO] ILE LEU LYS ALA ASN ALA ILE THR THR ILE LEU ALA [ALA] VAL THR PHE
 ATGGAGTTTGCCAAATCCCTCAAAAGCAAAATGCAAAATACCAACAATCCCTGCTGCAAGTCACATTT
 TACCTCAACGGTTAGGAGTTTTCGTTTACGTTTAAATGGTGTTAGGAGCGACGTCAGTGTA
 10 20 30 40 50 60

CYS PHE ALA [SER] SER GLN ASN ILE THR GLU GLU PHE TYR GLN SER THR CYS SER ALA VAL
 TGCTTTTGCTTCTAGTCAAAACATCACTGAAGAATTTTATCAATCAACATGCGAGTCAGTT
 ACGAAACGAAGATCAGTTTGTAGTGACTTCTTAAATAAGTTAGTTGTACGTCACGTCACAA
 70 80 90 100 110 120

SER LYS GLY TYR LEU SER ALA LEU ARG THR GLY TRP TYR THR SER VAL ILE THR ILE GLU
 AGCAAAAGGCTATCTTAGTGCTCTAAGAACTGGTTGGTATACCTAGTGTATTATAACTATAGAA
 TCGTTTCCGATAGAAATCACGAGATTCTTTGACCAACCAATATGATCAACAATATTGATATCTT
 130 140 150 160 170 180

LEU SER ASN ILE LYS GLU ASN LYS CYS ASN GLY THR ASP ALA LYS VAL LYS LEU [MET] LYS
 TTAAGTAATATCAAGGAATAAATAGTGTAATGGAAACAGATGCTAAGGTAATAAATTGATGAA
 AATTCAATTATAGTTTCCCTTTTATTCACATTTACCTTGCTACGATTCCCAATTTTAACTACTTT
 190 200 210 220 230 240

GLN GLU LEU ASP LYS TYR LYS ASN ALA VAL THR GLU LEU GLN LEU MET GLN SER THR
 CAAGAAATTAGATATAATAAATAATGCTGTAAACAGAAATGCGAGTTGCTCATGCAAGCACA
 GTTCTTAATCTATTATATTTTACGACATTGTCTTAACGTCACGAGTACGTTTCGTGT
 250 260 270 280 290 300

PRO [ALA] [ALA] ASN ASN ARG ALA ARG ARG GLU LEU PRO ARG PHE MET ASN TYR THR LEU ASN
 CCAAGCAGCAACAATCGAGCCAGAAAGAGAACTACCAAGGTTTATGAAATTATACACTCAAC
 GGTCTGTCGTTTGTAGCTCGGTCCTTCTCTTGATGGTTCCAAATACCTTAATAATGAGTTG
 310 320 330 340 350 360



F2-F1 CLEAVAGE SITE

ASN [THR] LYS LYS THR ASN VAL THR LEU SER LYS LYS ARG LYS ARG ARG PHE LEU GLY PHE
AATACCAAAACCAATGTAACATTAAGCAAGAAAGAAAGATTTCTTGTTT
TTATGGTTTCTTGGTTACATTTGTAATTCGTTCTTTTCTTTCTTAAAGAACCAAAA
370 380 390 400 410 420

LEU LEU GLY VAL GLY SER ALA ILE ALA SER GLY [ILE] ALA VAL SER LYS VAL LEU HIS LEU
TTGTTAGGTGTTGGATCTGCAATCGCCAGTGCCATTGCTGTATCTAAGGTCCTGCACTTA
AACAAATCCACAACCTAGACGTTAGCGGTCACCGTAACGACATAGATTTCCAGGACGTGAAT
430 440 450 460 470 480

GLU GLY GLU VAL ASN LYS ILE LYS SER ALA LEU LEU SER THR ASN LYS ALA VAL VAL SER
GAAGGAGAGTGAACAGATCAAAAGTGCTCTACTATCCACAACAAGCCGTCAGT
CTTCCCTCTTCACTTGTCTTAGTTTTCACGAGATGATAGGTTTGTTCGGGCATCAGTCA
490 500 510 520 530 540

LEU SER ASN GLY VAL SER VAL LEU THR SER LYS VAL LEU ASP LEU LYS ASN TYR ILE ASP
TTATCAAAATGGAGTTTAGTGCTTTAACCAAGCAAGTGTTAGACCTCAAAACCTATATAGAT
AATAGTTTACCTCAATCAACAGAAATTGGTCTGTTTCACAATCTGGAGTTTGTGATATATCTA
550 560 570 580 590 600

LYS GLN LEU LEU PRO ILE VAL ASN LYS ARG SER CYS [ARG] ILE SER ASN ILE GLU THR VAL
AAACAAATTGTTTACCCTATTGTTGAATAAGCGAAGCTGCAAGATATCAAAATATAGAACTGTG
TTTGTAAACAAATGGATAACACCTTATTTCGCTTCGACGTCCTTATAGTTTATATCTTTGACAC
610 620 630 640 650 660

ILE GLU PHE GLN HIS LYS ASN ASN ARG LEU LEU GLU ILE THR ARG GLU PHE SER VAL ASN
ATAGAGTTTCCAAACACAAGAAACAACAGACTACTAGAGATTACCAAGGAAATTTAGTGTAAAT
TATCTCAAGGTTGTGTTCTTGTGTTGTTGATGATCTCTAAATGGTCCCTTAAATCACAATTA
670 680 690 700 710 720

ALA GLY VAL THR THR PRO VAL SER THR TYR MET LEU THR ASN SER GLU LEU SER LEU
GCAGGTGTAACTACACCTGTAAAGCACTTACATGTTAACTAATAGTGAATTAATTGTCATTA
CGTCCACATTTGATGTGGACATTCGTGAATGTACAAATTGATTATCACTTAATAACAGTAAT
730 740 750 760 770 780

FIG.5B.



ILE ASN ASP MET PRO ILE THR ASN ASP GLN LYS LYS LEU MET SER ASN VAL GLN ILE
ATCAATGATATGCCCTATAACAATAATGATCAGAAAAAGTTAATGTCCAAACAATGTTCAAATA
TAGTTACTATAACGGATATTGTTTACTAGTCTTTTTCAAATTACAGGTTGTTACAAGTTTAT 840
790 800 810 820 830

VAL ARG GLN GLN SER TYR SER ILE MET SER ILE LYS GLU VAL LEU ALA TYR VAL
GTTAGACAGCAAAAGTTACTCTATCATGTCCTAATAAAGAGGAAAGTCTTTAGCATATGTA
CAATCTGTCGTTTCAATGAGATAGTACAGGTATTATTTTCTCCTTCAGAAATCGTATACAT 900
850 860 870 880 890

VAL GLN LEU PRO LEU TYR GLY VAL ILE ASP THR PRO CYS TRP LYS LEU HIS THR SER PRO
GTACAAATTACCACTATATGGGTGTGATAGATACACCTTGTGTGGAATAATACACACATCCCCCT
CATGTTAAATGGTGATATACCACTATCTATGTGGAACCAACCTTTAAATGTGTGTAGGGGA 950
910 920 930 940 950

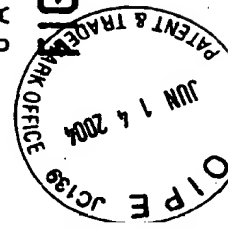
LEU CYS THR THR ASN THR LYS GLY GLY SER ASN ILE CYS LEU THR ARG THR ASP ARG GLY
CTATGTACAACCAACAAGAAAGGGTCAACATCTGTGTTTAAACAAGAACTGACAGAGGA
GATACATGTTGGTGTGTTTCTTCCAGTTTGTAGACAAATTTGTTCTTGACTGTCTCCT 1020
970 980 990 1000 1010

TRP TYR CYS ASP ASN ALA GLY SER VAL SER PHE PHE PRO GLN ALA GLU THR CYS LYS VAL
TGGTACTGTGACAAATGCAGGATCAGTATCTTTCTTCCCAACAAGCTGAACAATGTAAAGTT
ACCATGACACTGTTACGTCCTAGTCATAGAAAGAGGGTGTTCGACTTTGTACATTTCAA 1080
1030 1040 1050 1060 1070

GLN SER ASN ARG VAL PHE CYS ASP THR MET ASN SER LEU THR LEU PRO SER GLU VAL ASN
CAATCGAATCGAGTATTTTGTGACACAATGAAACAGTTTAAACATTAACCAAGTGAAAGTAAAT
GTTAGCTTAGCTCATAAAACACACTGTGTTACTTGTCAAAATTGTAATGGTTCACTTCATTTA 1140
1090 1100 1110 1120 1130

LEU CYS ASN VAL ASP ILE PHE ASN PRO LYS TYR ASP CYS LYS ILE MET THR SER LYS THR
CTCTGCAATGTTGACATATTCAATCCCAAAATATGATTTGTAATAATATGACTTCAAAAACA
GAGACGTTACAACCTGTATTAAGTTAGGGTTTATACTAACCATTTTAAATACTGAAGTTTGT 1200
1150 1160 1170 1180 1190

FIG. 5C.



ASP VAL SER SER SER VAL ILE THR SER LEU GLY ALA ILE VAL SER CYS TYR GLY LYS THR
GATGTAAGCAGCTCCGTTATACATCTCTAGGAGCCATTGTGTCATGCTATGGCAAACT 1250
CTACATTCGTCGAGGCAATAGTGTAGAGATCCCTCGGTAACACAGTACGATACCGTTTGA 1260
1210 1220 1230 1240 1250

LYS CYS THR ALA SER ASN LYS ASN ARG GLY ILE ILE LYS THR PHE SER ASN GLY CYS ASP
AAATGTACAGCATCCCAATAAATAATCGTGGAATCATAAAGACATTTTCTAACGGGTGTGAT 1320
TTTACATGTCTCGTAGGTTATTTTATAGCACCTTAGTATTTCTGTAAAGATTGCCCACACTA 1330
1270 1280 1290 1300 1310 1320

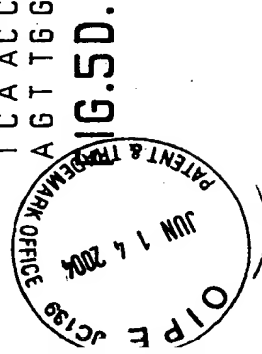
TYR VAL SER ASN LYS GLY VAL ASP THR VAL SER VAL GLY ASN THR LEU TYR TYR VAL ASN
TATGTATCAATAAAGGGGTGGACACTGTGTCGTAGGTACACATTTATATATTATGTAAT 1380
ATACATAGTTTATTTCCCCACCTGTGACACAGACATCCCATTTGTAAATATAATACATTTA 1390
1330 1340 1350 1360 1370 1380

LYS GLN GLU GLY LYS SER LEU TYR VAL LYS GLY GLU PRO ILE ILE ASN PHE TYR ASP PRO
AAGCAAGAAAGGCAAAAGTCTCTATGTAAAGGGTGAAACCAATAATAATTTCTATGACCCCA 1440
TTCGTTCTTCCGTTTTCAGAGATACATTTTCCACTTGGTTATTTTAAAGATACTGGGT 1450
1390 1400 1410 1420 1430 1440

LEU VAL PHE PRO SER ASP GLU PHE ASP ALA SER ILE SER GLN VAL ASN GLU LYS ILE ASN
TTAGTATTTCCCTCTCTGATGAAATTTGATGCAATCAATACTCAAGTCAACGAGAGATTAAAC 1500
AATCATAAAGGGGAGACTACTTAACCTACGTAGTTATAGAGTTTCAGTTGCTCTTCTAATTG 1510
1450 1460 1470 1480 1490 1500

GLN SER LEU ALA PHE ILE ARG LYS SER ASP GLU LEU LEU HIS ASN VAL ASN ALA GLY LYS
CAGAGTTTAGCATTATTCGTAAATCCGATGAATTTATACATAATGTAAATGCTGGTAATA 1560
GTCTCAAAATCGTAAATAAGCATTTAGGCTACTTAATAATGTATTACATTTACGACCATTT 1570
1510 1520 1530 1540 1550 1560

SER THR THR ASN ILE MET ILE THR THR ILE ILE ILE GLU ILE ILE VAL ILE LEU LEU SER
TCA ACCACAAATATCATGATAACTACTATAATTAAGAGATTATAGTAATAATTGTTATCA 1620
AGTTGGTGTATTATAGTACTATTGATGATTAATAATCTCTAAATCATTAACAATAGT 1630
1570 1580 1590 1600 1610 1620



LEU ILE ALA VAL GLY LEU LEU LEU TYR CYS LYS ALA ARG SER THR PRO VAL THR LEU SER
 TTAATTGCTGTTGGACTGCTCCTATACTGTAAAGGCCAGAACACACCAAGTCACACCTAAGC
 AATTACGACAAACCTGACGAGGATATGACATTCCGGTCTTCCGTGTCAGTGTGATTCG 1680
 1630 1640 1650 1660 1670 1680
 LYS, ASP GLN LEU SER GLY ILE ASN ASN ILE ALA PHE SER ASN
 AAGGATCAACTGAGTGGTATATAATAATATTGCAATTTAGTAACCTGAAATAAATAAGCACCT
 TTCCTAGTTTGACTCACCATATTTATTATAACGTAAATCATTGACTTATTTTATTCGTGGA 1740
 1690 1700 1710 1720 1730 1740
 AATCATGTTCTTTACAATGGTTTACTATCTGCTCATAGACAACCACTCTATCATTTGGATTT
 TTAGTACAAGAAATGTTACCAAATGATAGACGAGTATCTGTTGGGTAGATAGTAACCTAAA 1800
 1750 1760 1770 1780 1790 1800
 TCTTAAAAATCTGAACCTTCATCGAAACTCTTATCTATATAAACCACTCTCACTTACACTATTTA
 AGAATTTTAGACTTTGAAGTAGCTTTTGAGAAATAGATATTGTTAGGTAGAGTGAAATGTGATAAAT 1850
 1810 1820 1830 1840 1850 1860
 AGTAGATTCCCTAGTTTATAGTTATAT 3'
 TCATCTAAGGATCAAAATATCAATATA 1870
 1870 1880

NUCLEOTIDE SEQUENCE OF THE RSV F GENE. THE CDNA SEQUENCE IS SHOWN IN THE PLUS (mRNA)
 STRAND SENSE IN THE 5' TO 3' DIRECTION. THE SIGNAL PEPTIDE (SP) AND THE TRANSMEMBRANE (TM)
 ANCHOR DOMAIN ARE UNDERLINED. THE PREDICTED F2-F1 CLEAVAGE SITE IS INDICATED BY THE ARROW
 (↓). AMINO ACIDS DIFFERING FROM THE PUBLISHED PRIMARY SEQUENCE OF THE PROTEIN ENCODED BY
 THE RSV F GENE ARE BOXED.

FIG. 5E.



RESTRICTION MAP OF THE RSV F GENE

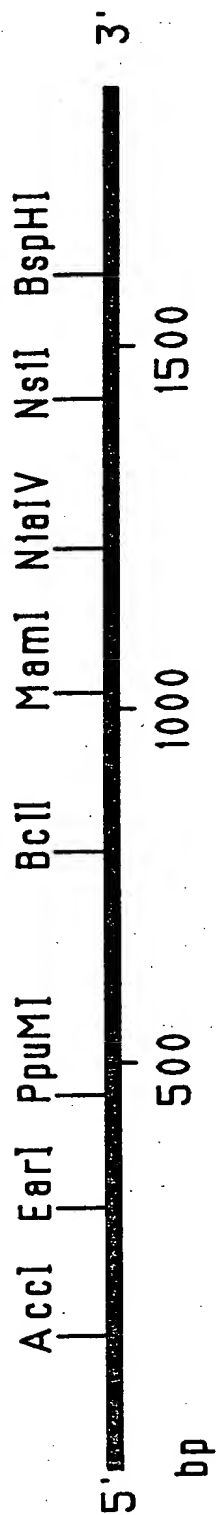


FIG.6.



FIG.7A.

NUCLEOTIDE SEQUENCE OF THE RSV G GENE

MET SER LYS ASN LYS ASP GLN ARG
T G C A A A C A T G T C C A A A A A C A A G G A C C A A C G
A C G T T T G T A C A G G T T T T T G T T C C T G G T T G C
10 20 30

THR ALA LYS THR LEU GLU **LYS** THR TRP ASP
C A C C G C T A A G A C A C T A G A A A A G A C C T G G G A
G T G G C G A T T C T G T G A T C T T T T C T G G A C C C T
40 50 60

THR LEU ASN HIS LEU LEU PHE ILE SER SER
C A C T C T C A A T C A T T T A T T A T T C A T A T C A T C
G T G A G A G T T A G T A A A T A A T A A G T A T A G T A G
70 80 90

GLY LEU TYR LYS LEU ASN LEU LYS SER VAL
G G G C T T A T A T A A G T T A A A T C T T A A A T C T G T
C C C G A A T A T A T T C A A T T T A G A A T T T A G A C A
100 110 120

TM

ALA GLN ILE THR LEU SER ILE LEU ALA MET
A G C A C A A A T C A C A T T A T C C A T T C T G G C A A T
T C G T G T T T A G T G T A A T A G G T A A G A C C G T T A
130 140 150

ILE ILE SER THR SER LEU ILE ILE **THR** ALA
G A T A A T C T C A A C T T C A C T T A T A A T T A C A G C
C T A T T A G A G T T G A A G T G A A T A T T A A T G T C G
160 170 180

ILE ILE PHE ILE ALA SER ALA ASN HIS LYS
C A T C A T A T T C A T A G C C T C G G C A A A C C A C A A
G T A G T A T A A G T A T C G G A G C C G T T T G G T G T T
190 200 210

VAL THR **LEU** THR THR ALA ILE ILE GLN ASP
A G T C A C A C T A A C A A C T G C A A T C A T A C A A G A
T C A G T G T G A T T G T T G A C G T T A G T A T G T T C T
220 230 240

ALA THR SER GLN ILE LYS ASN THR THR PRO
T G C A A C A A G C C A G A T C A A G A A C A C A A C C C C
A C G T T G T T C G G T C T A G T T C T T G T G T T G G G G
250 260 270

THR TYR LEU THR GLN **ASP** PRO GLN LEU GLY
A A C A T A C C T C A C T C A G G A T C C T C A G C T T G G
T T G T A T G G A G T G A G T C C T A G G A G T C G A A C C
280 290 300



FIG.7B.

ILE SER **PHE** SER ASN **LEU** SER GLU ILE THR
 A A T C A G C T T C T C C A A T C T G T C T G A A A T T A C
 T T A G T C G A A G A G G T T A G A C A G A C T T T A A T G
 310 320 330

SER GLN **THR** THR THR ILE LEU ALA SER THR
 A T C A C A A A C C A C C A C C A T A C T A G C T T C A A C
 T A G T G T T T G G T G G T G G T A T G A T C G A A G T T G
 340 350 360

THR PRO GLY VAL LYS SER **ASN** LEU GLN **PRO**
 A A C A C C A G G A G T C A A G T C A A A C C T G C A A C C
 T T G T G G T C C T C A G T T C A G T T T G G A C G T T G G
 370 380 390

THR THR VAL LYS THR LYS ASN THR THR THR
 C A C A A C A G T C A A G A C T A A A A A C A C A A C A A C
 G T G T T G T C A G T T C T G A T T T T T G T G T T G T T G
 400 410 420

THR GLN THR GLN PRO SER LYS PRO THR THR
 A A C C C A A A C A C A A C C C A G C A A G C C C A C T A C
 T T G G G T T T G T G T T G G G T C G T T C G G G T G A T G
 430 440 450

LYS GLN ARG GLN ASN LYS PRO PRO **ASN** LYS
 A A A C A A C G C C A A A A C A A A C C A C C A A A C A A
 T T T T G T T G C G G T T T T G T T T G G T G G T T T G T T
 460 470 480

PRO ASN ASN ASP PHE HIS PHE GLU VAL PHE
 A C C C A A T A A T G A T T T T C A C T T C G A A G T G T T
 T G G G T T A T T A C T A A A A G T G A A G C T T C A C A A
 490 500 510

ASN PHE VAL PRO CYS SER ILE CYS SER ASN
 T A A C T T T G T A C C C T G C A G C A T A T G C A G C A A
 A T T G A A A C A T G G G A C G T C G T A T A C G T C G T T
 520 530 540

ASN PRO THR CYS TRP ALA ILE CYS LYS ARG
 C A A T C C A A C C T G C T G G G C T A T C T G C A A A A G
 G T T A G G T T G G A C G A C C C G A T A G A C G T T T T C
 550 560 570

ILE PRO ASN LYS LYS PRO GLY LYS LYS THR
 A A T A C C A A A C A A A A A A C C A G G A A A G A A A A C
 T T A T G G T T T G T T T T T T G G T C C T T T C T T T T G
 580 590 600



FIG.7C.

THR THR LYS PRO THR LYS LYS PRO THR PHE
C A C C A C C A A G C C T A C A A A A A A C C A A C C T T
G T G G T G G T T C G G A T G T T T T T T T G G T T G G A A
610 620 630

LYS THR THR LYS LYS ASP **LEU** LYS PRO GLN
C A A G A C A A C C A A A A A A G A T C T C A A A C C T C A
G T T C T G T T G G T T T T T T C T A G A G T T T G G A G T
640 650 660

THR THR LYS **PRO** LYS GLU VAL PRO THR THR
A A C C A C T A A A C C A A A G G A A G T A C C C A C C A C
T T G G T G A T T T G G T T T C C T T C A T G G G T G G T G
670 680 690

LYS PRO THR GLU GLU PRO THR ILE ASN THR
C A A G C C C A C A G A A G A G C C A A C C A T C A A C A C
G T T C G G G T G T C T T C T C G G T T G G T A G T T G T G
700 710 720

THR LYS THR ASN ILE **THR** THR THR LEU LEU
C A C C A A A A C A A A C A T C A C A A C T A C A C T G C T
G T G G T T T T G T T T G T A G T G T T G A T G T G A C G A
730 740 750

THR **ASN** ASN THR THR GLY ASN PRO **LYS** LEU
C A C C A A C A A C A C C A C A G G A A A T C C A A A A C T
G T G G T T G T T G T G G T G T C C T T T A G G T T T T G A
760 770 780

THR SER GLN MET GLU THR PHE HIS SER THR
C A C A A G T C A A A T G G A A A C C T T C C A C T C A A C
G T G T T C A G T T T A C C T T T G G A A G G T G A G T T G
790 800 810

SER SER GLU GLY ASN **LEU** SER PRO SER GLN
C T C C T C C G A A G G C A A T C T A A G C C C T T C T C A
G A G G A G G C T T C C G T T A G A T T C G G G A A G A G T
820 830 840

VAL SER THR THR SER GLU **HIS** PRO SER GLN
A G T C T C C A C A A C A T C C G A G C A C C C A T C A C A
T C A G A G G T G T T G T A G G C T C G T G G G T A G T G T
850 860 870

PRO SER SER PRO PRO ASN THR **THR** ARG GLN
A C C C T C A T C T C C A C C C A A C A C A A C A C G C C A
T G G G A G T A G A G G T G G G T T G T G T T G T G C G G T
880 890 900



G TAGTTATTAAAAA
CATCAATAATTTT
910 920

NUCLEOTIDE SEQUENCE OF THE RSV G GENE. THE cDNA
SEQUENCE IS SHOWN IN THE PLUS (mRNA) STRAND
SENSE IN THE 5' TO 3' DIRECTION. THE TRANSMEMBRANE
(TM) ANCHOR DOMAIN IS UNDERLINED. AMINO ACIDS
DIFFERING FROM THE PUBLISHED PRIMARY SEQUENCE OF
THE PROTEIN ENCODED BY THE RSV G GENE ARE BOXED.

FIG.7D.



RESTRICTION MAP OF RSV G GENE

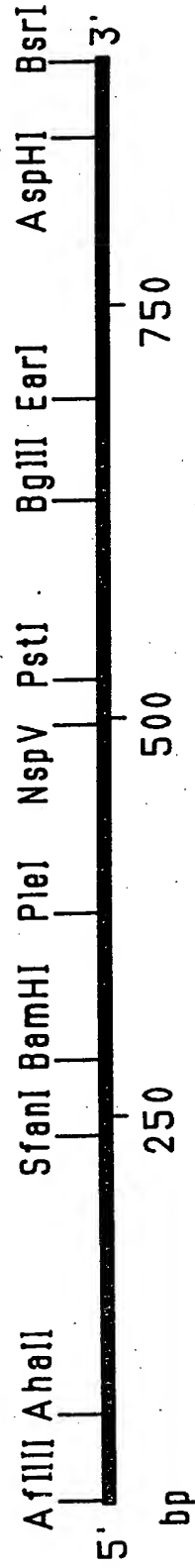


FIG.8.



Construction of a Bluescript-based expression vector containing the chimeric F_{PIV-3} -F_{RSV} gene with the 5' untranslated region of the PIV-3 F gene intact but lacking the nucleotide sequences coding for the hydrophobic anchor domains and cytoplasmic tails of both the PIV-3 and RSV F genes.

Step 1: Preparation of the plasmid containing the modified PIV-3 F gene

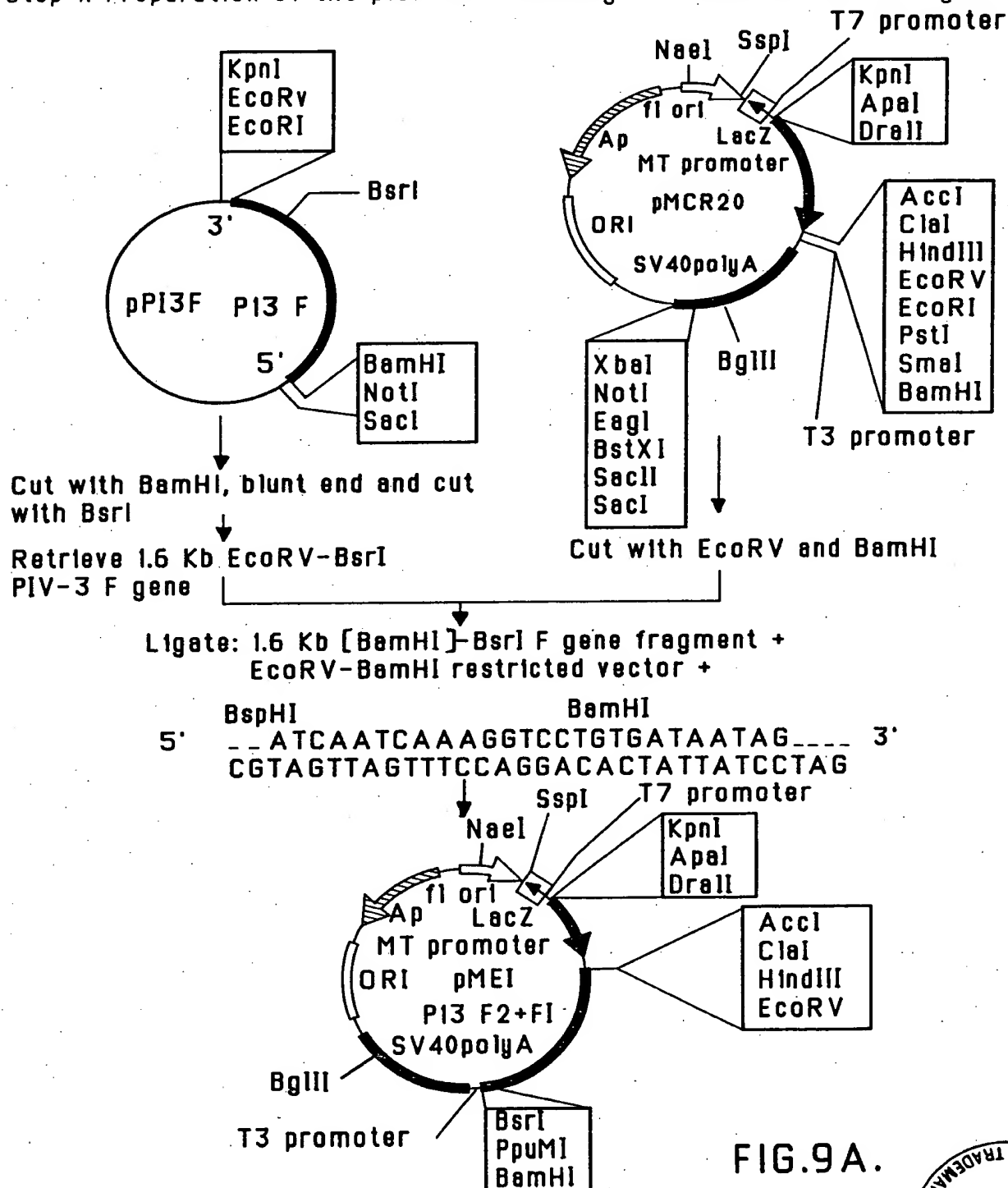
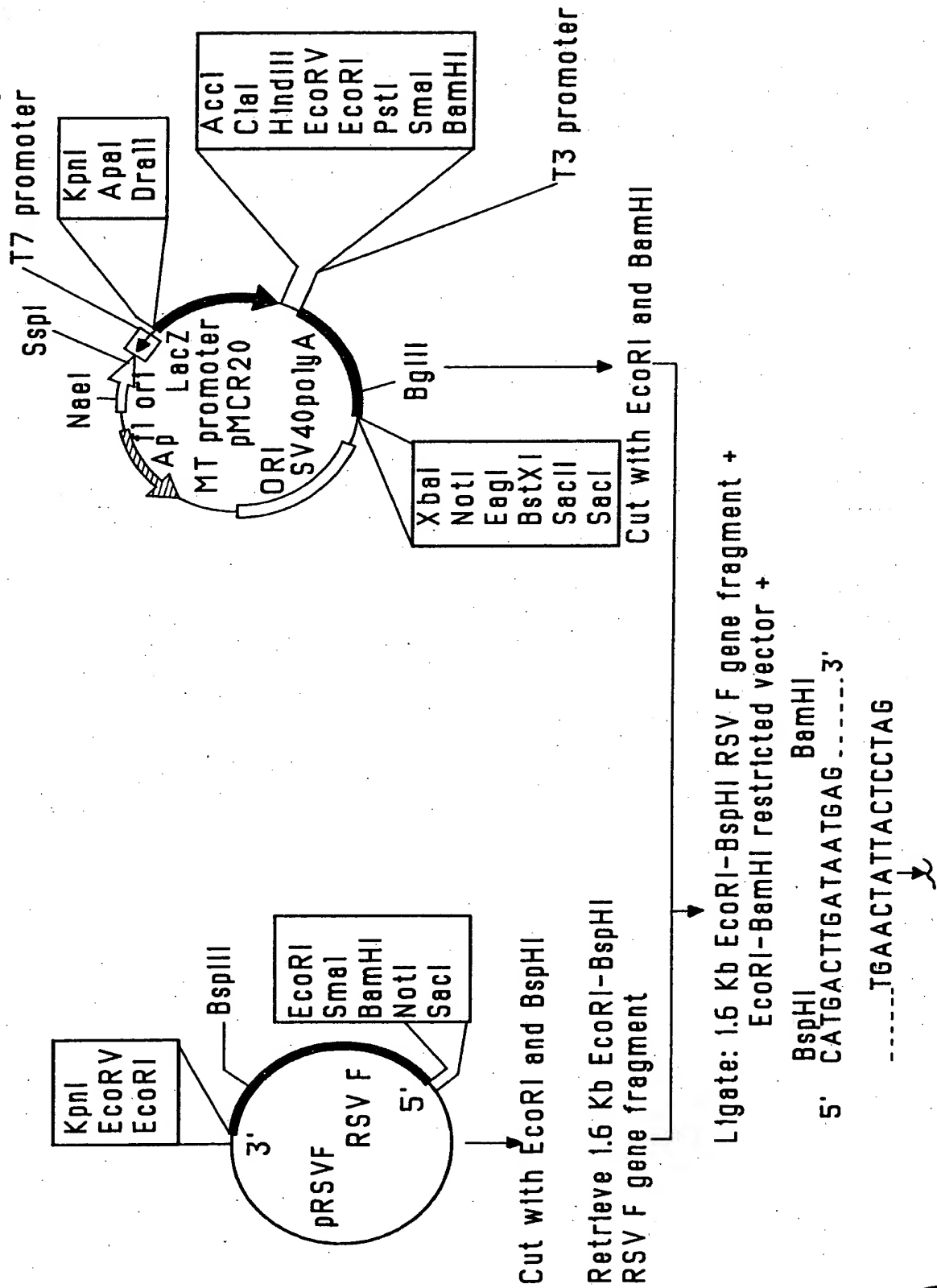


FIG.9A.



FIG.9B.

Step 2: Preparation of the plasmid containing the modified RSV F gene



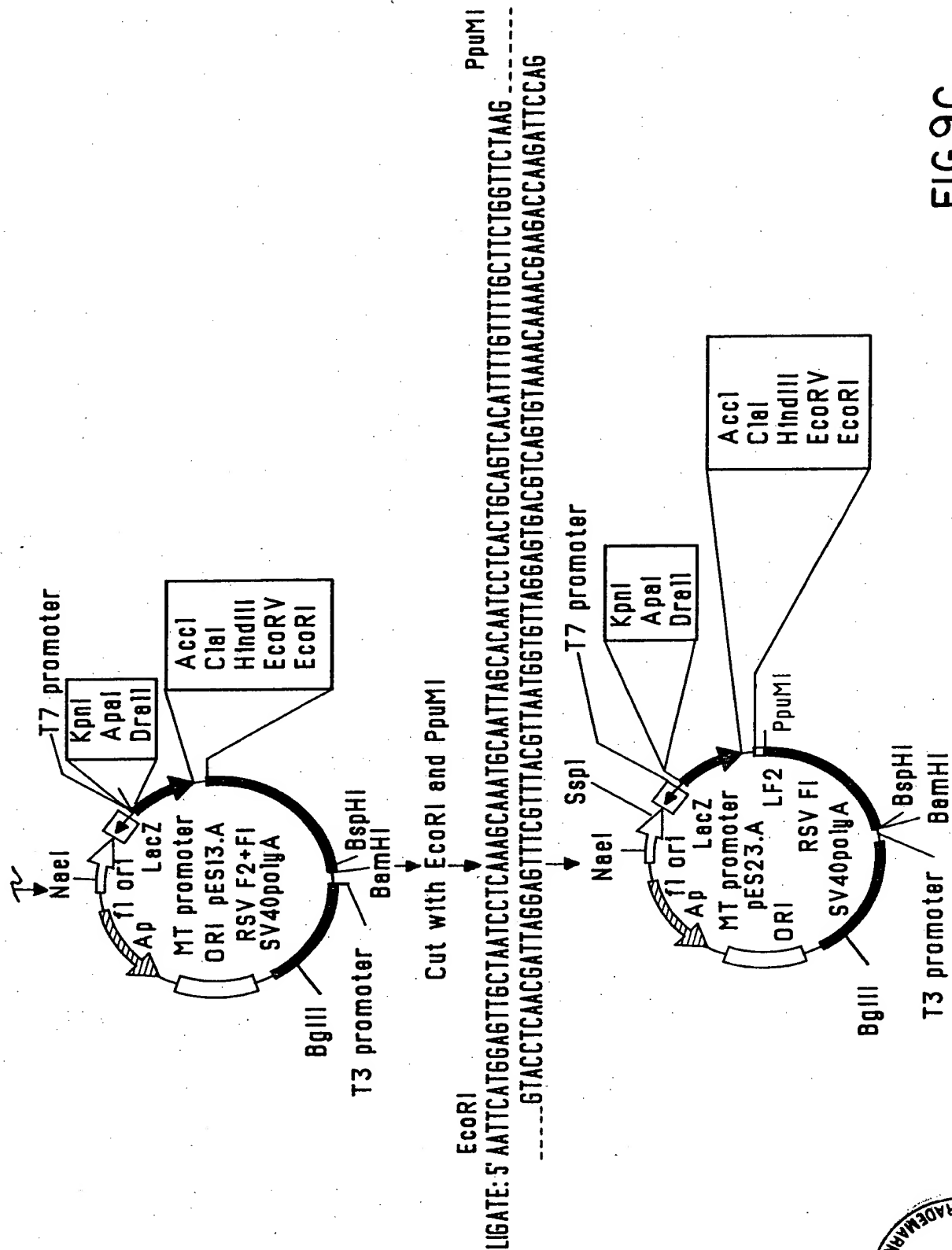


FIG.9C.



Step 3 : Preparation of the plasmid containing the chimeric FpIV-3 -F RSV gene

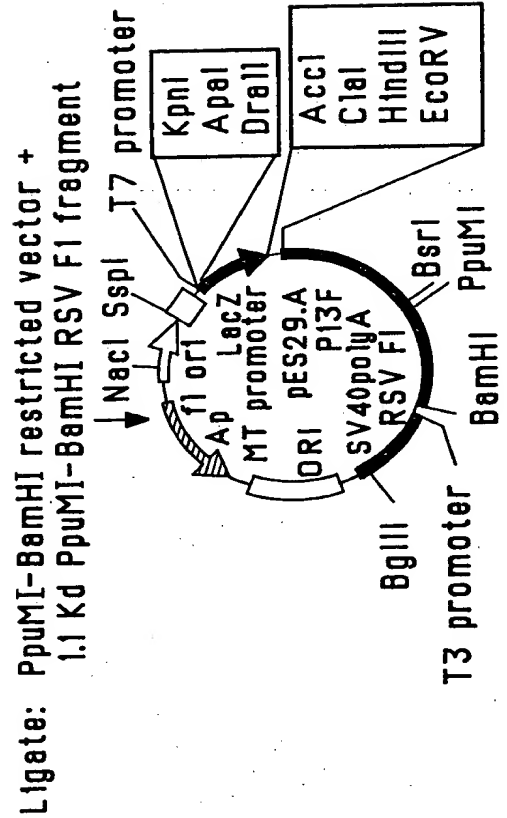
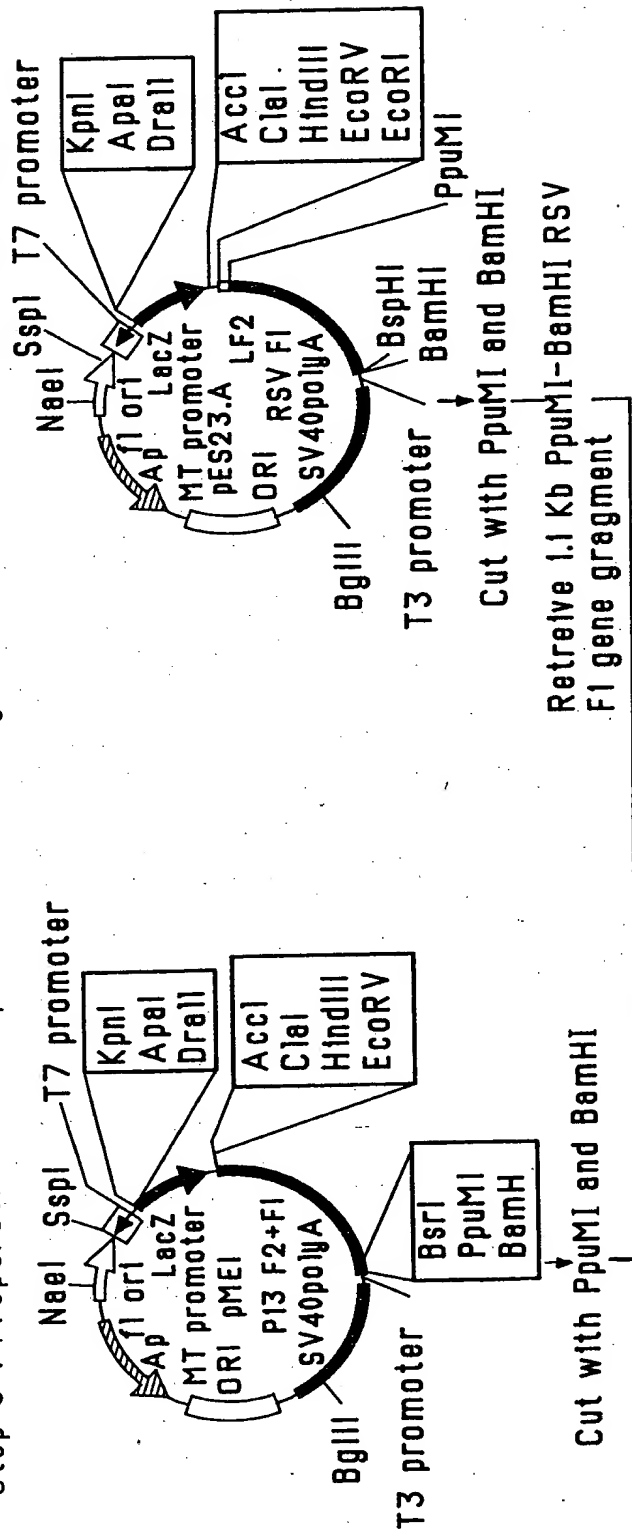


FIG.9D.

Construction of a Bluescript-based expression vector containing the PIV-3 F gene lacking the 5' untranslated sequence and transmembrane anchor and cytoplasmic tail coding regions.

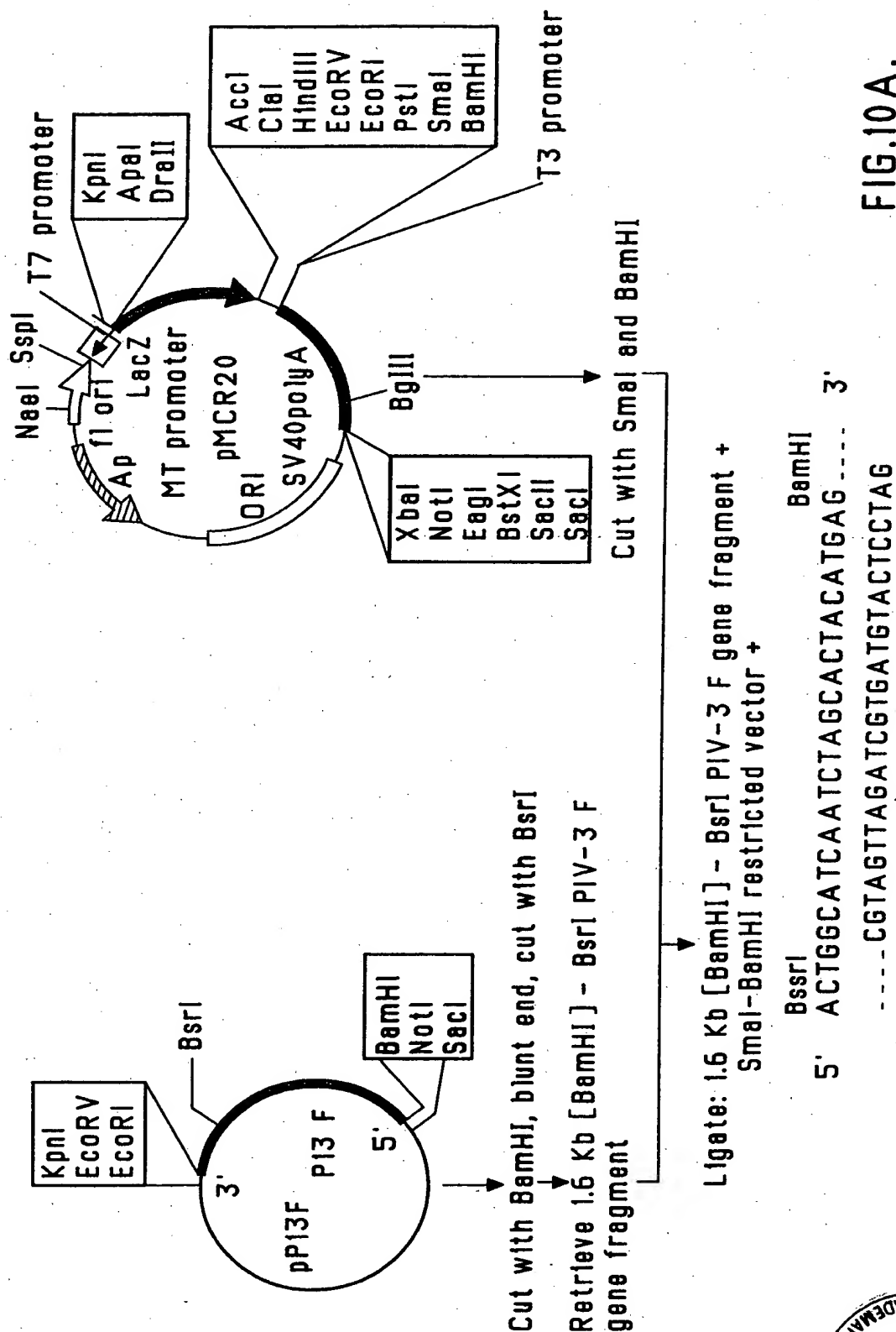
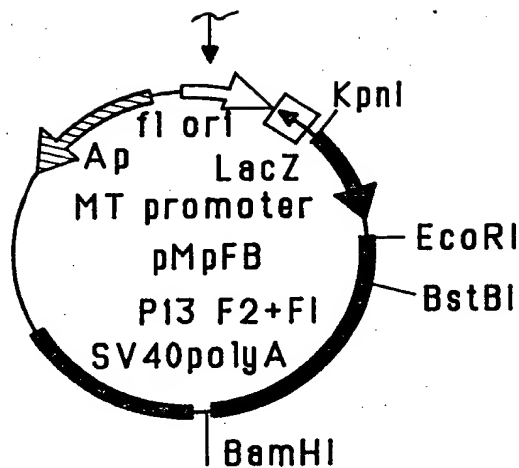


FIG.10A.



FIG.10B.



Cut with EcoRI and BstBI

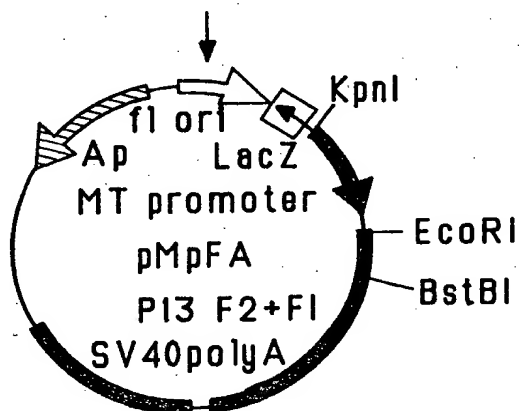
Retrieve: EcoRI-BstBI restricted vector

Ligate: EcoRI-BstBI restricted vector +

EcoRI

PpuMI

AATTCATGCCAACTTTAATACTGCTAATTATTACAACAATGATTATGG
 CATCTTCCTGCCAAATAGATATCACAAAACCTACAGCAATGTAGGTGTA
 TTGGTCAACAGTCCCAAAGGGATGAAGATATCACAAAACCTT _ _ _ _ 3'
 _ _ _ _ GTACGGTTGAAATTATGACGATTAATAATGTTGTTACTAATACC
 GTAGAAGGACGGTTTATCTATAGTGTTTTGATGTCGTACATCCACATA
 ACCAGTTGTCAGGGTTTCCCTACTTCTATAGTGTTTTGAAGCTT



Construction of the chimeric FPIV-3-FRsv gene consisting of the truncated PIV-3 F gene devoid of the 5' untranslated region linked to the truncated RSV F1 gene.

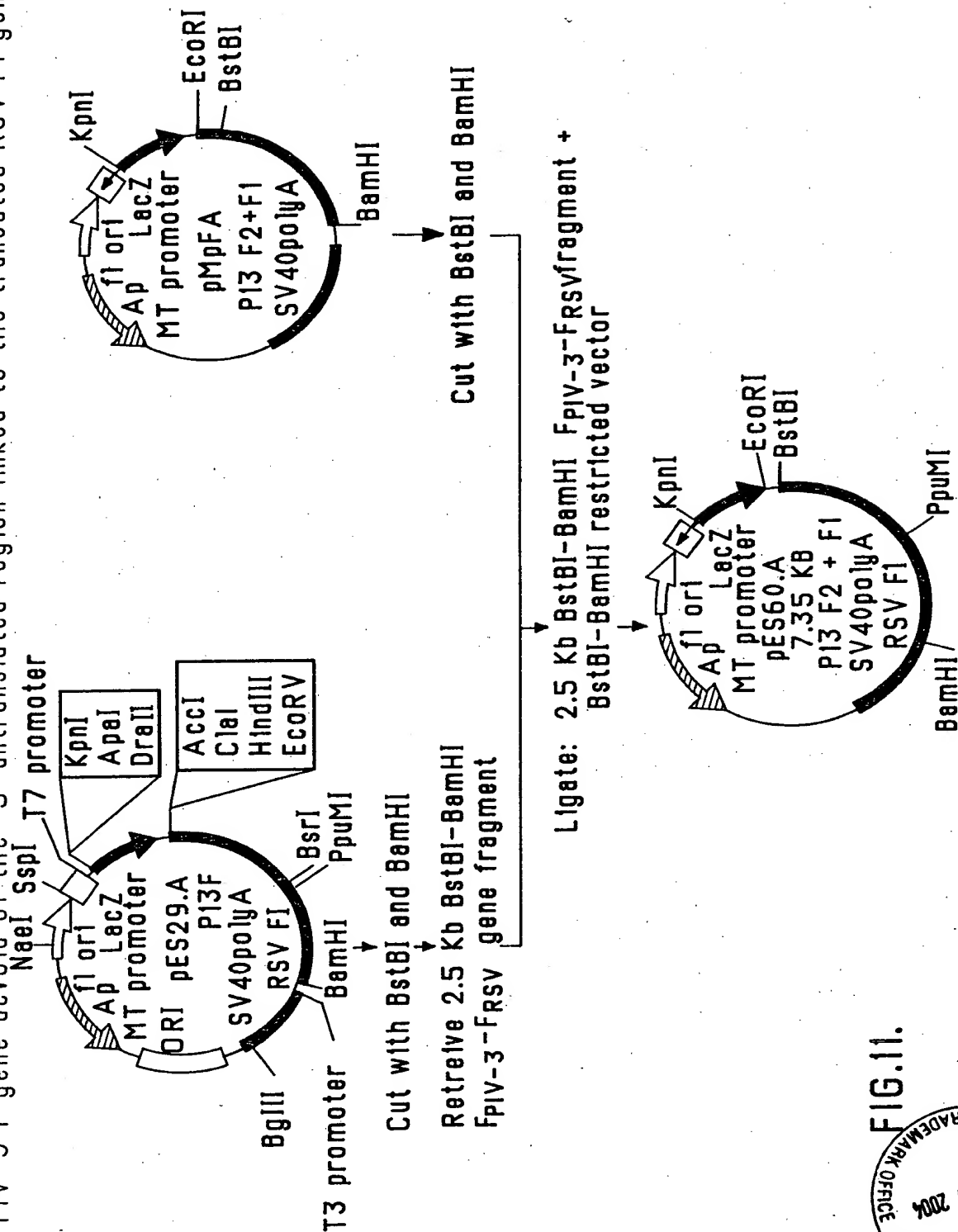
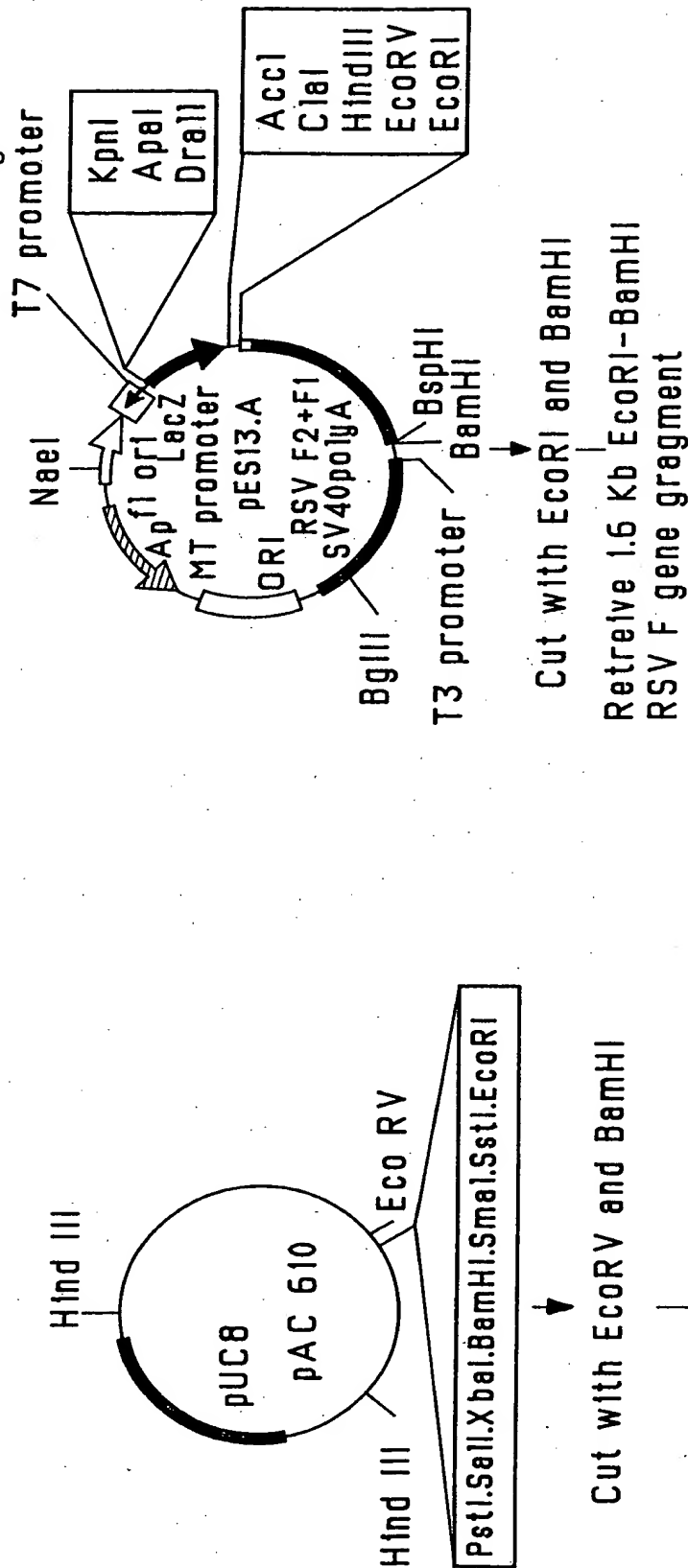


FIG.11.



FIG.12A.

Construction of the modified pAc 610 baculovirus expression vector containing the chimeric Fpiv-3-FRSV gene consisting of the PIV-3 F gene lacking both the 5' untranslated sequence as well as the transmembrane and cytoplasmic tail coding regions linked to the truncated RSV F1 gene



Ligate: 1.6 Kb EcoRI-BamHI RSV F gene fragment +
EcoRV-BamHI restricted vector +
EcoRV

5' ATCATGGAGATAATTAAGTACCATCTCGCAATAAATAAGTATTTTACIGTTTTGTAACAGTTTTGTAATAAANAACCTATAATAG 3'
TAGTACCTCTATTAAATTTTACTATTGGTAGAGCGTTTATTATTCATAAATGACANAAGCATTGTGCAAAACATTATTTTTTGGATATTATCTTAA



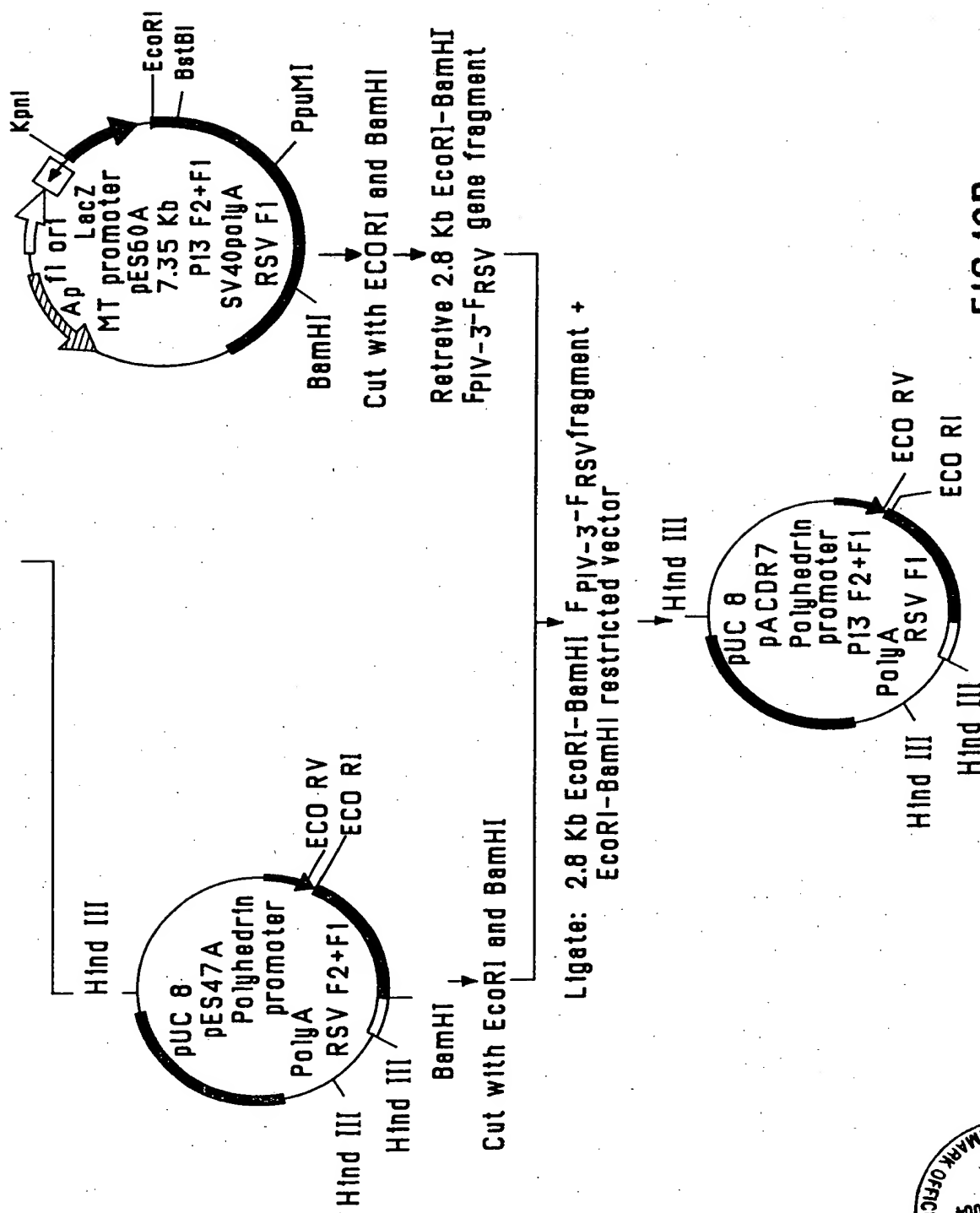


FIG.12B.

FIG.13

**IMMUNOBLOTS OF CELL LYSATES FROM Sf9 CELLS
INFECTED WITH RECOMBINANT BACULOVIRUSES**

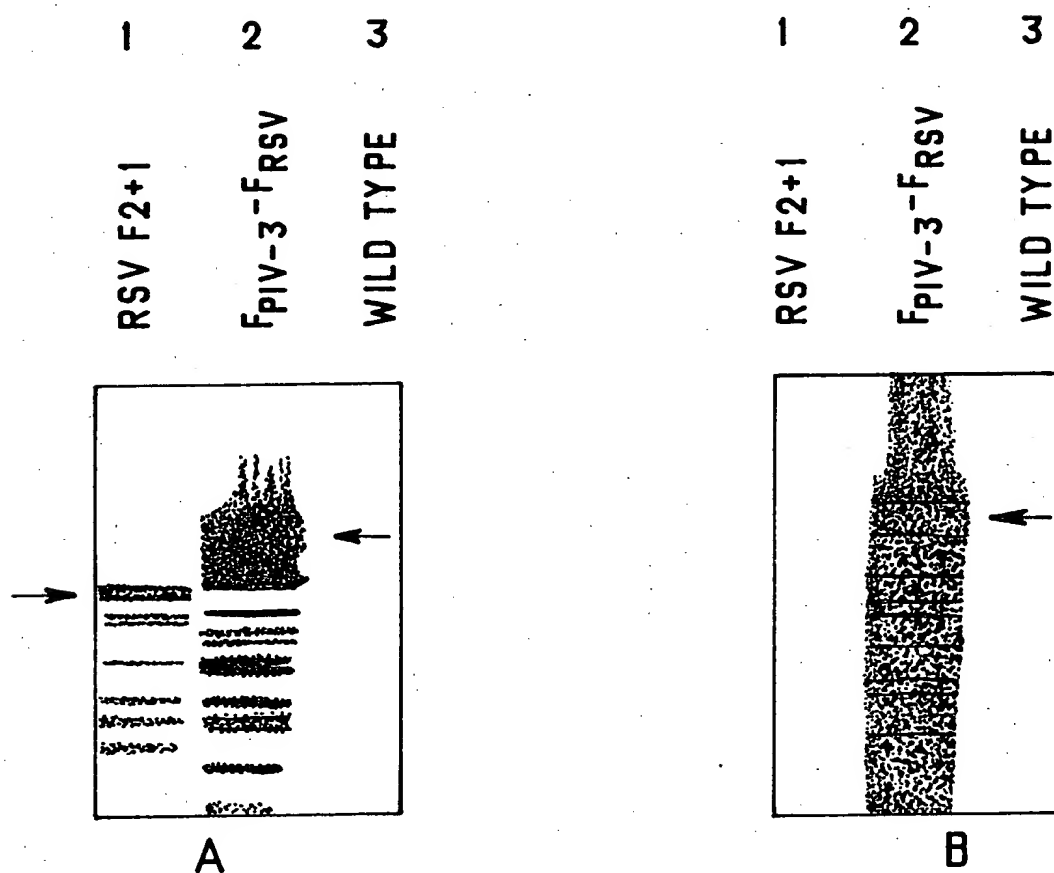


FIG 13 : Immunoblots of cell lysates from Sf9 cells infected with recombinant baculoviruses containing the truncated RSV F gene (Lane 1), the chimeric F_{PIV-3}-F RSV gene (Lane 2) or infected with wild type virus (Lane 3) reacted with anti-F RSV Mab (panel A) and anti-F1 PIV-3 antiserum (panel B)

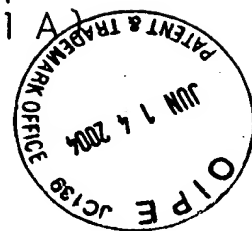


FIG.14. CONSTRUCTION OF THE BACULOVIRUS TRANSFER VECTOR pD2

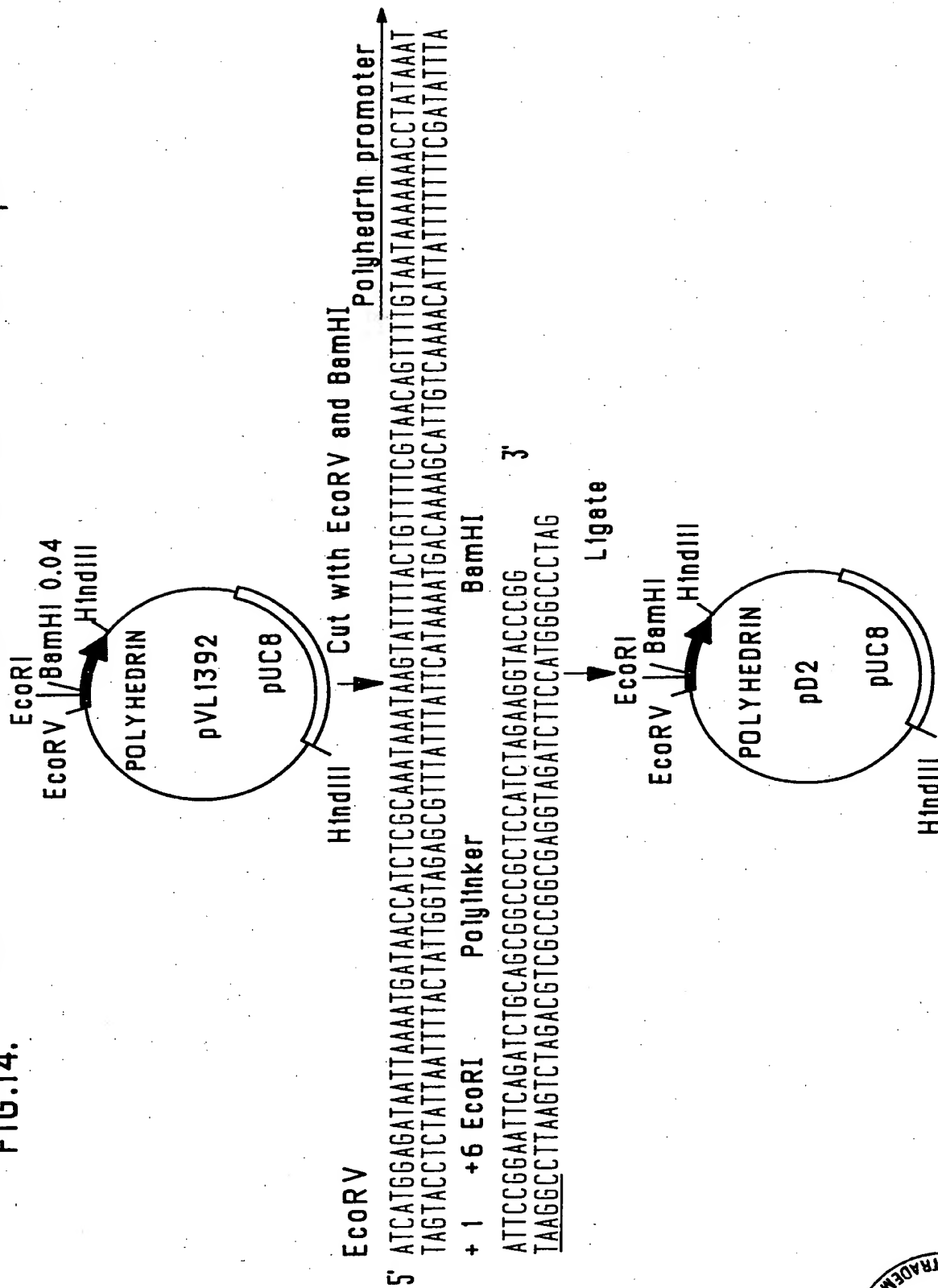


FIG.15A. CONSTRUCTION OF THE $F_{RSV-HN_{PIV3}}$ CHIMERIC GENE

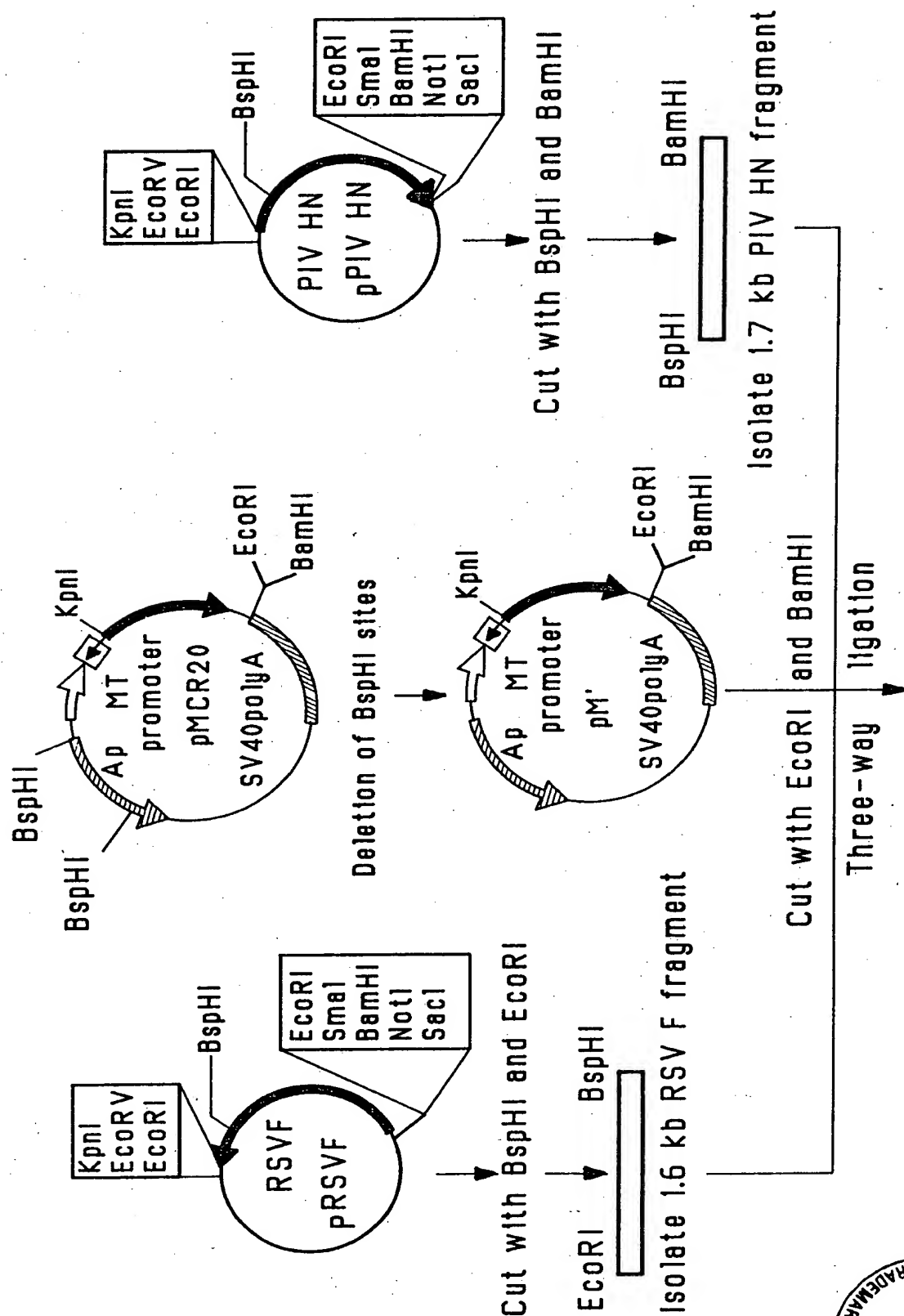


FIG.15B.

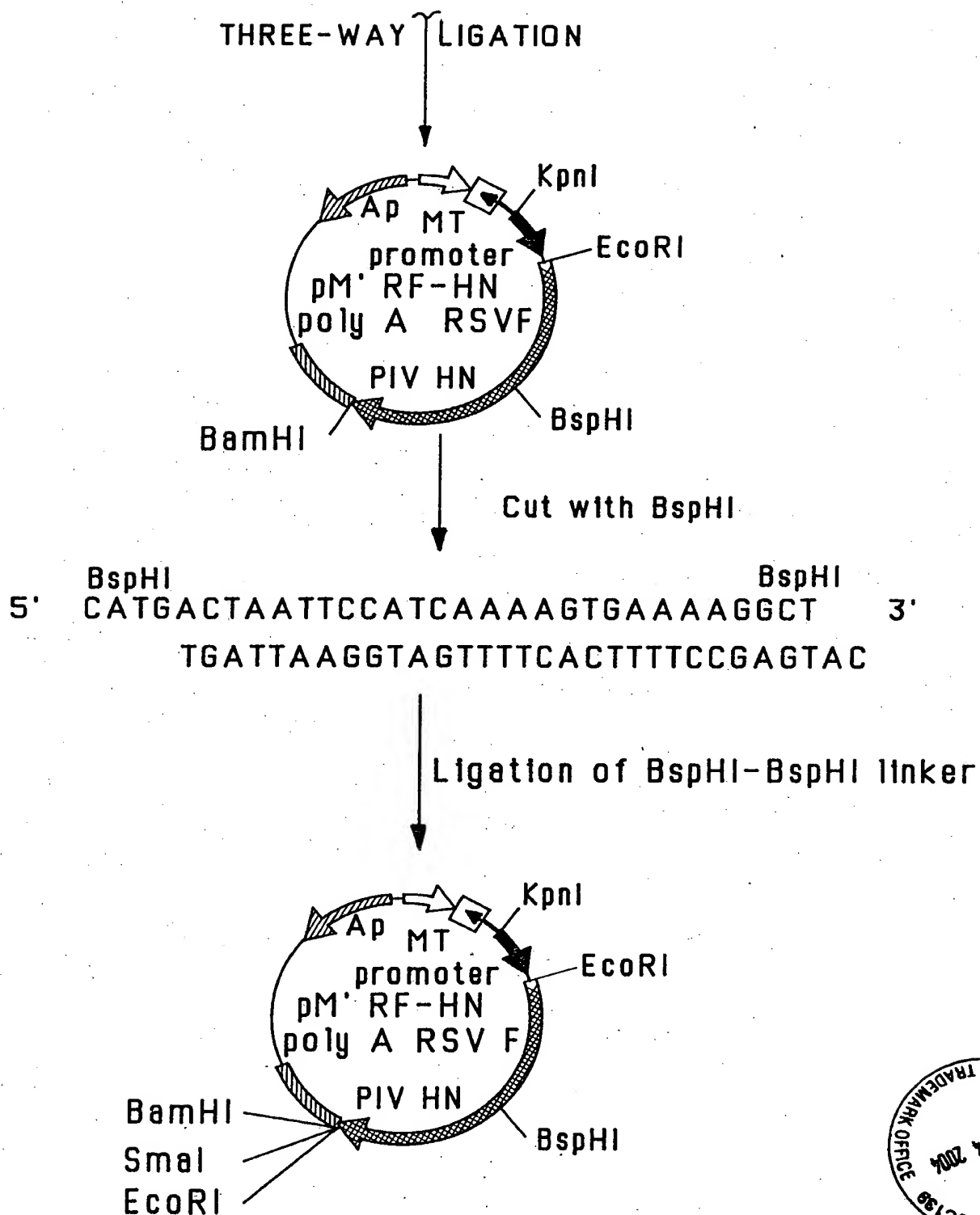


FIG.16

SDS POLY ACRYLAMIDE GEL AND IMMUNOBLOTS OF
PURIFIED F_{RSV} - HN_{PIV-3} CHIMERIC PROTEIN

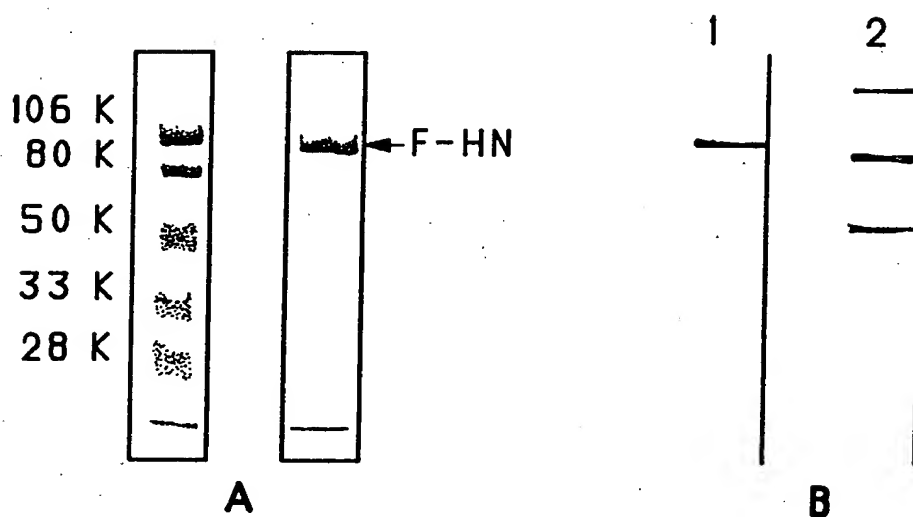


FIG 16 : A) Coomassie-stained SDS polyacrylamide gel of immunoaffinity- purified F_{RSV} - HN_{PIV-3} protein.

B) Immunoblots of F_{RSV} - HN_{PIV-3} protein reacted with an anti-F RSV Mab (lane 1) and anti-HN PIV-3 antiserum (lane 2)



FIG.17. MUTAGENESIS OF THE PIV-3 F GENE

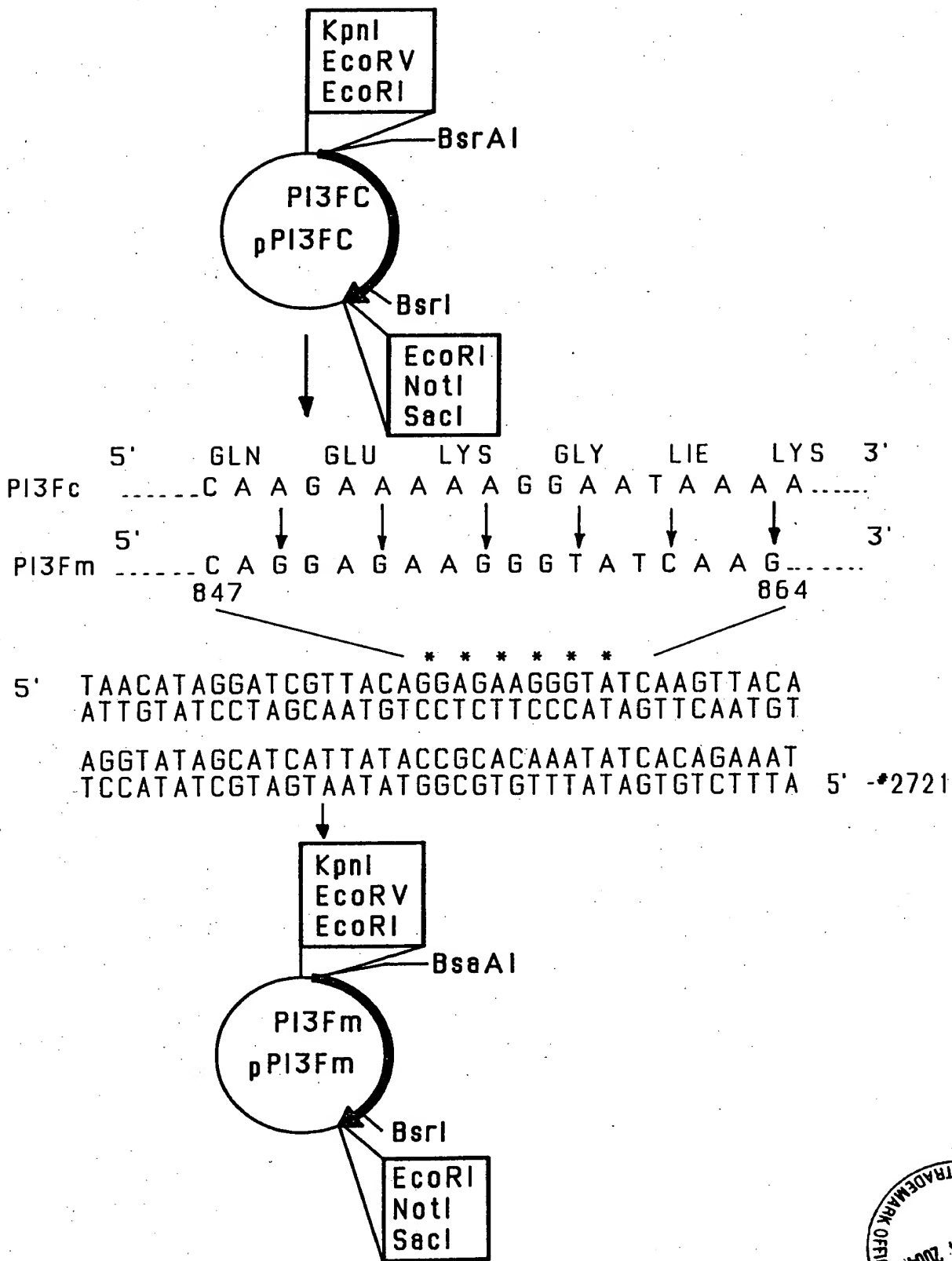


FIG.18. CONSTRUCTION OF THE F_{PIV3}-G_{RSV} CHIMERIC GENE

